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Olivo N., Ramos A., Schable C. Lal R.B., Holmberg S.D., Ernet J.A.;
Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernet J.A.;
"Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic-
diversity in the United States.";
J. Infect. Dis. 18:470-475(2000).
EMBL; AF190955; A602317.1;
GO; GO:0016021; C:infegral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
                           Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R., Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A., Calazans A.R., Tanuri A.;
Calazans A.R., Tanuri A.;
Cancarans A.R., Tanuri A.;
Cenchyping and phenotyping analysis of B and non-B Human immunodeficiency virus type 1 subtypes from patients under HAART.";
Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, API65561; AAPR08506.1;
GO; GO:0016021; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral molecule activity; IEA.
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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SUllivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,

A Sullivan F.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,

A Sullivan F.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,

A Sullivan F.J., Do A., Ellenberger D.L., Paul S., Kalish M.,

A Jones J., Ward J.;

T "Surveillance of Central African Nationals living in the United States

T reveals multiple subcypes of HIV-1 Group M and Group O.";

Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

I Shamitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:integral to membrane; IEA.

RO; GO:0019031; C:integral to membrane; IEA.

RO; GO:0019031; C:integral to membrane; IEA.

RO; GO:0005198; Pstructural molecule activity; IEA.

R InterPro; IPR000328; Brv_GP41.
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                                                                                                                                                                                                                                                                  Length 117;
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117 AA; 13986 MW; 4719FD6EB98E42E3 CRC64;
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro: IPR000328; Env_GP41.
PF00517; GP41; 1.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Pred. No. 1.3e-13;
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Best Local Similarity 100.0%; Pred. No. 1.3
Matches 26; Conservative 0; Mismatches
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Esteves A., Parreira R., Venenno T., Franco M., Piedade J.,
Germano de Sousa J., Canas-Ferreira W.;
"Genetic diversity of HIV-1 spreding among intravenous drug users in
Lisbon, Portugal.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ429041; CAD23677.1; -.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000328; Entuctural molecule activity; IEA.
InterPro; IPR000328; Entuctural molecule activity; IEA.
NON TER 12 123
NON TER 12 123
SEQÜENCE 123 AA; 14895 MW; 489C41C5C275D88F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Swanson P.A., Devare S.G., Hackett J.R. Jr.,
"Molecular Characterization of 39 HIV-1 Isolates Representing Group I (Subbypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY214095; AA061815.1;
GO; GO:0109131; C:viral envelope, IEA.
InterPro; IPR000128; Extructural molecule activity; IEA.
PF00517; GP41; 1.
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
Virus_TaxID=11676;
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tive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 26; Conservative
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Q7ZJR4;
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STRAIN-GH8;
Pienlazek D., Yang C., Lal R.L.;
Pienlazek D., Yang C., Lal R.L.;
"Phylogenetric analysis of gp41 envelope of HIV-1 groups M, N, and O isolates provides an alternate region for subtype determination.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF113589; AAD42757.1; -.
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Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
Rayfield M.;
Rayfield M.;
"HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0015031; C:integral to membrane; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPRO00328; Env_GP41:
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Pred. No. 1.4e-13;
Mismatches 0; Indels 0;
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122 AA; 14703 MW; 09E2E31B37786D34 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein immunodominant region (Fragment).
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; Fstructural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
PF00517; GP41; 1.
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Matches 26; Conservative 0; Mismatches
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Q72C48
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX185383; AA065658.1;
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
FRANCE: PRR000328; Env. GP41: 1.
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STRANT=RLUKS3-2;
Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
"Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naive patients infected with subtype B
and non-B HIV-1.";
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144 AA; 16887 MW; Al39DlC53D318EBE CRC64;
                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                 Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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  1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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                          17 RILAVERYLKDOQLLGIWGCSGKLIC
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SEQUENCE 144 AA;
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                                                                                  Length 144;
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Subhitted (NOV-2002) to the EMBL/GenBank/DDBJ databages.
EMBL, AY185468; AA065743.1;
GO; GO:0019931; C:viral envelope; IEA.
HINE-EMPLY IRROBOUSES; Envertural molecule activity; IEA.
InterPro: IRROBOUSE; Env GP41.
Envelope protein..
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
144 144
144 AA; 16907 MW; A427C02C24218EEB CRC64;
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145 AA; 17020 MW; ACBC32E97B09D1A1 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Pred. No. 1.6e-13;
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Local Similarity 100.0%; Pred. No. 1.6
es 26; Conservative 0; Mismatches
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Steuler H., Storch-Hagenlocher B., Wildemann B.;
"Distinct populations of Human immunodeficiency virus type 1 in blood and cerebrospinal fluid.";
AIDS Res. Hum. Retroviruses 8:53-59(1992).
EMBL; X61356; CAA43624.1; -..
EMBL; X61356; CAA43624.1; -..
EMBL; S3591; A53591.
FIR, A53591; CAA3591.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
PFam; PF00517; GP41; 1.
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MEDLINE=92144209; PubMed=1736940;
Steuler H., Storch-Hagenlocher B., Wildemann B.;
Steuler B., Storch-Hagenlocher B., Mildemann B.;

"Distinct populations of Human immunodeficiency virus type 1 in blood and cerebrospinal fluid.";
AIDS Res. Hum. Retroviruses 8:53-59(1992).

EMBL, X61369; CAA43630.1;

PIR, S21998; S21998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 139; DB 15; Length 357; 100.0%; Pred. No. 4.1e-13; ive 0; Mismatches 0; Indels 0;
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SEQUENCE 358 AA; 41402 MW; E5E438667785A10D CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
Inter:PO:0005198; Env_GP41.
Pfam; PF00517; GP41; 1.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-NOV-1996 (TrEMBLrel. 01, Last seg
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Best Local Similarity 100.0
Matches 26; Conservative
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SEQUENCE
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Q78120;
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145 AA; 17003 MW; 9CC7F8CD12FBD430 CRC64;
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18393 MW; DE623EDD88411EC3 CRC64;
EMBL; AY185472; AAO65747.1; -. GO:0019931; C:viral envelope; IEA. GO:0019931; C:viral envelope; IEA. GO:00051998; F:structural molecule activity; IEA. BITCEPPC; PRO00328; ENV GP41. Pfam; PF00517; GP41; 1. ENVELOPE protein. 1 1 NON TER 145 145
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J. Virol. 76:7595-7606(2002).
GMBL; AJ428022; CAD20974.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                            Score 139; DB 15;
Pred. No. 1.6e-13;
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Pred. No. 1.7e-13;
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0; Mismatches
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100.0%; Pred. No. 1.
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-UUN-2003 (TrEMBLrel. 24, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                               26; Conservative
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Best Local Similarity 100.
Matches 26; Conservative
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155 AA;
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 26; Conserv
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Q78119;
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                                                                                                                                                                                                                                                                                                                              Envelope glycoprotein (Fragment).
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Matches 26; Conservative
                                                                                                                     PRELIMINARY;
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SEQUENCE
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A DCOSTA S.S., Hurwitz J.L.;

ERCOSTA S.S., Hurwitz J.L.;

ERCOSTA
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                                                                                                                                                                                                                                                                                                                                                                                             GO, GO:0016021, C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019131, C:viral envelope; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP120; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15; Length 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 15; Length 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coat protein; Glycoprotein; Polyprotein; Transmembrane.
                                                                                                                                                                                                                                               of HIV-1.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                     DCOsta S.S., Hurwitz J.L.;
"Escape mutants to determine structure of gp120 of HIV-1
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF321147; AAK20295.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65643 MW; 47475A5780240AE8 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                         Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 139; DB 15;
Pred. No. 7e-13;
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Pred. No. 7e-13;
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- Human immunodeficiency virus 1.
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Best Local Similarity 100.0%;
Matches 26; Conservative 0
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Best Local Similarity 100.0
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                                                                                                                                                               SEQUENCE FROM N.A.
                                                                       NCBI_TaxID=11676;
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DCOSta S.S., Hurwitz J.L.;

DCOSta S.S., Hurwitz J.L.;

DCOSta S.S., Hurwitz J.L.;

Escape mutants to determine structure of gp120 of HIV-1.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AR32146; AAK20294.1; ---

R PIR, AS3591, AS3591.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0019021; C:integral to membrane; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R Interpro; IPR000328; Env. GP41.

R Interpro; IPR00077; GP120.

R Pfam; PF00516; GP120; 1.

R Pfam; PF00516; GP120; 1.

R AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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A DCOSETS S.S., Hurwitz J.L.;
ESCAGADE mutents to determine structure of gp120 of HIV-1.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
L. Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
R. EMBL; AF321144; AAK20292.1; -.
R. PIR; A53591; A53591.
R. GO; GO:0016021; C:integral to membrane; IEA.
R. GO; GO:0019028; C:viral capsid; IEA.
R. GO; GO:0019031; C:viral envelope; IEA.
R. GO; GO:0019031; C:viral envelope; IEA.
R. GO; GO:005198; F:structural molecule activity; IEA.
R. InterPro; IPR000228; ENV. GP41.
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                       Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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1 RILAVERYLKDQQLLGIWGCSGKLIC 26
   EMBL; AF321143; AAK20291.1; -.
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ses 26; Conservative
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618
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                                                                            DB 15; Length 590;
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Escape mutants to determine structure of gpl20 of HIV-1."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF321145; AAK20293.1; -. PIR; A53591; A53591.
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                                                                                                               Indels
                                     65902 MW; 91ED899CB8F91CAF CRC64;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0051989; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676;
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                                                                          100.0%; Score 139; DB 15;
100.0%; Pred. No. 7e-13;
iive 0; Mismatches 0;
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                                                            Query Match
Best Local Similarity 100.0
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nes 26; Conservative
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590 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Chaiken I., Hoxie J.A., Doms R.W.;
"Stable exposure of the coreceptor-binding site in a CD4-independent
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PIR; A53591; A53591.

GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:inteal capaid; IEA.
GO; GO:0019031; C:viral capaid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR00077; GP120.
Ffam; PF00516; GP120; 1.
Pfam; PF00516; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 727 AA; 82201 MW; P90FD626D26B9E6 CRC64;
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"Virol. 73:10310-10319, [1999].

EMBL, AF189158, AAF25627.1; -.

PIR, A53591; A53591.

GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

InterPro; IPR000777; GP120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 15, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Envelope polyprotein variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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; Pred. No. 8.7e-13;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. No. 7.3 ive 0; Mismatches
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MEDLINE=99272698; PubMed=10339592;
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MEDLINE=20027260; PubMed=10559349;
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Mulder K.E.;

Mulder K.E.;

Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.

BMBL; U12032; AAA76668.1; -.

PIR; A53591; AA3766.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019028; C:viral envelope; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0005198; F:seructural molecule activity; IEA.

R InterPro; IPR000328; Env GP41.

R InterPro; IPR00177; GP120.

R Pfam; PF00516; GP120; 1.

R Pfam; PF00517; GP41; 1.

M AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
         AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
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Matches 26; Conservative
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                                                                 SEQUENCE FROM N.A.
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                                                                                             STRAIN=LW881;
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SEQUENCE
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Shaw G., Kong L., Walss S., Waters D., Gallo R., Blattner W.;
"Wiral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HTLV type IIIB).";
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000777; GP41.
InterPro; IPR000777; GP120.
Pfam; PF00517; GP120, 1.
Pfam; PF00517; GP41; 1.
Pfam; PF00517; GP41; 1.
Pfam; PF00517; GP41; 1.
Pfam; PF00517; GP41; 1.
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Submitted (UUL-1994) to the EMBL/GenBank/DDBJ databases.
EMBL: 112034; AAA76669.1; -
PIR; A53591; A53591.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676,
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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; Pred. No. 8.9e-13;
0; Mismatches 0;
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574 RILAVERYLKDOOLLGIWGCSGKLIC 599
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STRAIN=LW87-1;
MEDLINE=95127297; PubMed=7826699;
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Best Local Similarity 100.0%;
Matches 26; Conservative 0
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STRAIN=LW851;
MEDLINE=95127297; PubMed=7826699;
MEDLINE=95127297; PubMed=7826699;
Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HTLV type IIIB).";
AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
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Pfam; PF00516; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
NON TER 752 A; 84894 MW; 8B30AE894013B45A CRC64:
                                                            DB 15; Length 748;
                                                      100.0%; Score 139; DB 15; Length 100.0%; Pred. No. 9e-13; ive 0; Mismatches 0; Indels
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Mulder K.E.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
748 AA; 84224 MW; 56BEDF186C67694B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       070604;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNN-2093 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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InterPro; IPR000625; REV_protein.
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    RET REPRESENT OF THE PROPERTY 
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WEDLINE=5512797; PubMed=7826699;
RELIZ M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HTLV type IIIB).";
AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
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Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:00109028; C:integral to membrane; IEA.
GO; GO:00139031; C:inteal capsid; IEA.
GO; GO:001399; F:structural molecule activity; IEA.
InterPro; IPR000328; Env G941.
InterPro; IPR000377; G9120.
Pfam; PF00516; GP120; 1.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41.
NAIDS; Coat protein; Glycoprotein; Transmembrane.
NON_TER 752 752
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Mulder K.E.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U12031; AAA76667.1; -.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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MEDLINE=95127297; PubMed=7826699;
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type 1 variant map outside regions required for coreceptor
T specificity.";
J. Virol. 73:10310-10319(1999).

E MBL; AF189159; AAP25628.1; -.

PIR; A53591; A53591; A53591 to membrane; IEA.

R GO; GO:00126021; C:integral to membrane; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019028; C:viral envelope; IEA.

R GO; GO:0019028; F:structural molecule activity; IEA.

R GO; GO:0003700; F:structural molecule activity; IEA.

R GO; GO:000328; F:structural molecule activity; IEA.

R GO; GO:000328; F:structural molecule activity; IEA.

R GO; GO:000328; Expendition of transcription, DNA-dependent; IEA.

R InterPro; IPR000377; GP120.
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MEDLINE=99272698; PubMed=10339592;
HOffman T.L., LaBranche C.C., Zhang W., Canziani G., Robinson J.,
Chalken I., Hoxie J.A., Doms R.W.;
"Stable exposure of the coreceptor-binding site in a CD4-independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LaBranche C.C., Hoffman T.L., Romano J., Haggarty B.S., Edwards T.G.,
Matthews T.J., Doms R.W., Hoxie J.A.;
"Determinants of CD4 independence for a human immunodeficiency virus
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                                                                                                                                                                                                                                                                     GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR00077; GP120, 1.
Ffam; PF00517; GP120, 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
NON_TER 752
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Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Envelope polyprotein variant.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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100.0%; Pred. No. 9e-13;
Micmatches 0;
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infected with HIV type 1 (HTLV type IIIB).";
AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
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Matches 26; Conserv
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Length 801;

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SEQUENCE FROM N.A.

A GOLTY P.R., Taylor J., Holm G., Mehle A., Morgan T., Cayabyab M.,

B Farzan M., Wang H., Bell J.B., Kunstman K.J., Moore J.P.,

Wolinsky S.M., Gabuzda D.;

"Increased CCRs affinity and reduced CCRs/CD4 dependence of a
"Increased CCRs affinity and reduced CCRs/CD4 dependence of a
neurovirulent primary human immunodeficiency virus type 1 isolate.";

J. Virol. 0:0-0(2002).

R EMBL; AF491740; AAM09793.1; -

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral capsid; IEA.

GO; GO:0019031; C:viral capsid; IEA.

GO; GO:0019031; P:structural molecule activity; IEA.

R InterPro; IPR000328; Env GP41.
                         Triques K., Bourgeois A., Saragosti S., Vidal N., Mpoudi-Ngole E. Nzilambi N., Apetrei C., Ekwalanga M., Delaporte E., Peeters M.; High diversity of HIV-1 subtype F strains in Central Africa."; Virology 259-99-108 (1999).

EMBL; AJ237807; CAB44058.1; -.

EMBL; AJ237807; CAB44058.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019021; C:viral capsid; IEA.

GO; GO:0019021; C:viral envelope; IEA.

GO; GO:0019031; C:viral envelope; IEA.

InterPro; IPR000777; GP120.

InterPro; IPR000777; GP120.
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Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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90521 MW; 9AEE71C1C840A88B CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 139; DB 15; Best Local Similarity 100.0%; Pred. No. 9.6e-13; Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              534 RILAVERYLKDQQLLGIWGCSGKLIC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RILAVERYLKDQQLLGIWGCSGKLIC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
            MEDLINE=99294894; PubMed=10364493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Envelope glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00516; GP120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              801 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00517;
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIDS; COA
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8Q2X2
Q8Q2X2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AIDS;
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Q9WMV0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triques K., Bourgeois A., Saragosti S., Vidal N., Mpoudi-Ngole E., Nzilambi N., Apetrei C., Ekwalanga M., Delaporte E., Peeters M.; "High diversity of HIV-1 subtype F strains in Central Africa."; Virology 259:99-109(1999).

EMBL, AJ237805; CAB44056.1; -. GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0019021; C:integral to membrane; IEA.

GO; GO:0019021; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

InterPro; IPR000328; ENG GF41.
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                                                                                                                                                                                      Length 757;
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Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
Pfam; PF00424; REV; 1.
AlDS; Coar protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 757 Aa; 85539 WW; A758AF8D8263BD2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope (Gp160) (Fragment).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UNV-1093 (TrEMBLrel. 24, Last annotation update)
Envelope (Gpl60) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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NCBI_TaxID=11676;
                                                                                                                                                                                   Query Match
100.0%; Score 139; DB 15;
Best Local Similarity 100.0%; Pred. No. 9.1e-13;
Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                533 RILAVERYLKDQQLLGIWGCSGKLIC 558
                                                                                                                                                                                                                                                                                                           1 RILAVERYLKDOQLLGIWGCSGKLIC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RILAVERYLKDOOLLGIWGCSGKLIC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus 1.
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SEQUENCE FROM N.A.
STRAIN=MP535;
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SEQUENCE
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Q9WMV1
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Q9WMU9
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Gaps
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                                                                                    Query Match 100.0%; Score 139; DB 15; Length 807; Best Local Similarity 100.0%; Pred. No. 9.7e-13; Matches 26; Conservative 0; Mismatches 0; Indels 0
Coat protein; Glycoprotein; Polyprotein; Transmembrane.
NCE 807 AA; 91808 MW; 4B52479155EF5603 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     809 AA
                                                                                                                                                                                                                                                  590 RILAVERYLKDQQLLGIWGCSGKLIC 615
                                                                                                                                                                                                          1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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Gaps

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Hahn B.H.; "Molecular cloning and analysis of functional envelope genes from human immunodeficiency virus type 1 sequence subtypes A through G.
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C STRAIN=95127;
A Montavon C., Delaporte E., Peeters M.;
Anotravon C., Delaporte E., Peeters M.;
Two new complete genomes of HIV-1 recombinant AGJ BFP90-like
Circulating in Mali and Senegal.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
BEML; AJ288982; CAB98175.1;
CO; GO:0019021; C:integral to membrane; IEA.
RG; GO:0019028; C:viral capsid; IEA.
RG; GO:0019031; C:viral envelope; IEA.
RG; GO:0019031; C:viral envelope; IEA.
RG; GO:0005198; F:scructural molecule activity; IEA.
RINGERPO; IPR000328; ENV GP41.
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Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,
von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
                                                                      Length 826;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane. SEQUENCE 845 AA; 95239 MW; 39439B37713EBD2A CRC64;
                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                   826 AA; 93694 MW; 344AF31B694B6883 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses, Retroid viruses; Retroviridae, Lentivirus
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
                                                              100.0%; Score 139; DB 15;
100.0%; Pred. No. 9.9e-13;
ive 0; Mismatches 0;
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Pred. No. 1e-12;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                               845 AA
                                                                                    100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              847 AA.
                                                                                                                                                                                                         1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus 1.
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                                                                                                                       26; Conservative
                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
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                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (
01-JUN-2003 (
ENV protein.
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                   SEQUENCE
                                                                      Query Match
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                                                                                                                       Matches
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Q9ID89
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X MEDLINE=99294894; PubMed=10364493;

A Triques K., Bourgeois A., Saragosti S., Vidal N., Mpoudi-Ngole E.,

A Triques K., Bourgeois A., Saragosti S., Vidal N., Mpoudi-Ngole E.,

Nailambi N., Apetrei C., Ekwalanga M., Delaporte E., Peeters M.;

Yi "High diversity of HIV-1 subtype F strains in Central Africa.";

XI Virology 259:99-109(1999).

BR MBL; AJ237806; CAB44057.1;

DR GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:001993; F:structural molecule activity; IEA.

InterPro; IPR000777; GP120.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                             Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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100.0%; Pred. No. 9.7e-13;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            542 RILAVERYLKDQQLLGIWGCSGKLIC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RILAVERYLKDOQLLGIWGCSGKLIC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                              Envelope (Gp160) (Fragment).
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ENV OR GP160.
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Pfam; PF00517; GP41; 1.
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Pfam; PF00517; GP41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         809 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                               ENV OR GP160
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Q9DVL1

RESULT 33

Matches

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Gaps

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96239 MW; 40BE606217AE2915 CRC64;
   849 AA;
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01-JUN-2003 (
   SEQUENCE
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Q90CI9
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A Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
A Foley B.T., Ndung'u T.P., Marlink R., Essex M.;
L Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF110967; AAD17078.1; --
EMBL; AF110967; AAD17078.1; --
EMBL; AF10997; C:integral to membrane; IEA.
GG; GG:0019028; C:viral capsid; IEA.
R GG; GG:0019028; C:viral capsid; IEA.
R GG; GG:0019028; F:ructural molecule activity; IEA.
R InterPro; IPR000328; Env GP41.
R InterPro; IPR000328; Env GP41.
R Pfam; PF00516; GP120.
R Pfam; PF00517; GP120.
R Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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STRAIN=C-96BW05.02;
MEDLINE=99214383; PubMed=10196340;
Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F., Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
WHO and NIAID Networks for HIV Isolation and Characterization."; J. virol. 70:1651-1657(1996).
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                                                                                                                             STRAIN=594;
NIAID/NIH DAIDS Variation Program;
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U08445; AAB04071.1; -.
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                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:00019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR00077; GP120.
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01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pfam; PF00517; GP41; 1.
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SEQUENCE
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Gaps
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MEDLINE=21342588; PubMed=11448170;
Carr J.K., Torimiro J.N., Wolfe N.D., Eitel M.N., Kim B.,
Sanders-Buell E., Jagodzinski L.L., Gotte D., Burke D.S., Birx D.L.,
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SEQUENCE PROM N.A.
STRAIN=C.96BW05.04;
MEDLINE=99214383; PubMed=10196340;
MEDLINE=99214383; PubMed=10196340;
MOVITENY V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
ESSEX M.;
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 849 AA; 95476 MW; 898B30FA6ECCE3DC CRC64;
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                 Length 849;
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EMBL: AF377956, AAK59195.1; -.

EMBL: AF377956, AAK59195.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IPR000328; ENV GP41.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein.
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Last annotation update)
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NCBI_TaxID=11676;
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    Score 139; DB 15;
Pred. No. 1e-12;
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100.0%; Pred. No. 1e-12;
ive 0; Mismatches 0;
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                                                            26; Conservative
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"Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from Botswana.";
                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

A POVITERY V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,

A NoviteRy V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,

A FOLEY B.T., Ndung'u T.P., Marlink R., Essex M.;

L Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AFI10968; AAD17084.1;

GO, GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0019031; C:viral molecule activity; IEA.

R InterPro; IPR00077; GP120.

R FRam; PF00516; GP120;

R Pfam; PF00517; GP41; 1.
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MEDLINE=20122179; PubMed=10659053;
Triques K., Bourgeois A., Vidale N., Mpoudi-Ngole E.,
Mulanga-Kabeya C., Nzilambi N., Torimiro N., Saman E., Delaporte E.,
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"Near-Tull-length genome sequencing of divergent African HIV type 1
subtype F viruses leads to the identification of a new HIV type 1
subtype designated K.";
AIDS Res. Hum. Retroviruses 16:139-151(2000).
BMBL, AJ249239; CABS58990.1; -.
GO; GO:0016021; C:integral to embrane; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral molecule activity; IEA.
InterPro; IPR000177; GP120.
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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04B8B7B30E7307CE CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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96145 MW;
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01-JUN-2003
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Triques K., Bourgeois A., Vidale N., Mpoudi-Ngole E.,
Mulanga-Kabeya C., Nzilambi N., Torimiro N., Saman E., Delaporte E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Near-full-length genome sequencing of divergent African HIV type 1 subtype F viruses leads to the identification of a new HIV type 1 subtype designated K.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Comparison of complete env gene sequences from individuals with
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Ataman-Onal Y., Coiffier C., Giraud A., Babic-Erceg A., Biron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 15; Length 851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00517; GP41; 1.*
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
NON_TER 1
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; Pred. No. 1e-12;
0; Mismatches 0; Indels
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1FA238916F5F8A96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIDS Res. "Hum. Retroviruses 16:139-151(2000).

EMBL, AJ749236; CAB58978.1; -

EMBL, AJ7492216; Cintegral to membrane, IEA.

GO; GO:0019021; C:integral to membrane, IEA.

GO; GO:0019031; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

InterPro; IPR000328; Env GP41.

InterPro; IPR000777; GP120.
                                                                                                                                                          (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                       Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-UUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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AIDS Res. Hum. Retroviruses 15:1035-1039(1999)
EMBL, AF041132; AAC02523.1; -
GO, GO:0016021; C:integral to membrane; IEA.
                                                                                                                          851 AA.
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1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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851 AA; 96591 MW;
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100.0%;
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Best Local Similarity 100.0
Matches 26, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
                                                                                                                        PRELIMINARY;
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                                                                                                                                                          01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
ENV protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Peeters M.;
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[1] SEQUENCE FROM N.A. STRAIN=NL4-3;
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01-JUN-2003
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Q72502
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QBUNLO
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MEDIJNE=92219406; PubMed=1373204;
MEDIJNE=92219406; PubMed=1373204;
Dai L.C., Littaua R., Takahashi K., Ennis F.A.;
"Mutation of human immunodeficiency virus type 1 at amino acid 585 on gp41 resultis in loss of killing by CD8+ A24-restricted cytotoxic T
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Production of acquired immunodeficiency syndrome-associated retrovirus in human and nonhuman cells transfected with an infectious
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=86281827; PubMed=3016298;
Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
Martin M.A.;
                                                                                                                                             Gaps
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:001918; F:structural molecule activity; IEA.
InterPro; IPR0001328; Env GP41.
InterPro; IPR000177; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
Pfam; PF00517; GP41; 1.
SEQUENCE 854 AA; 97062 MW; 58B012C83A0C3DA2 CRC64;
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ICE 854 AA; 97124 MW; ABAOA1BF36D5595A CRC64;
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                                                                                                                      Length
                                                                                                                                             Indels
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Submitted (JUL-1989) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0051989; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                    100.0%; Score 139; DB 15;
100.0%; Pred. No. 1e-12;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                    PRT;
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EMBL, M19921; AAA44992.1; -.
PIR, AS3591; AS3591.
PIR; S13288; S13288
                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecular clone.";
J. Virol. 59:284-291(1986)
                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 26; Conservative
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Pfam; PF00517; GP41; 1.
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Gaps
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Delgado E., Thomson M.M., Villahermosa M.L., Sierra M., Ocampo A.,
Miralles C., Rodriguez-Perez R., Diz-Aren J., Ojea-de-Castro R.,
Losada E., Cuevas M.T., Vazquez de Parga B., Carmona R.,
Perez Alvarez L., Medrano L., Cuevas L., Taboada J.A., Najera R.;
Tidentification of a newly characterized HIV-1 BG intersubtype
Circulating Recombinant Form in Galicia, Spain, exhibiting a
pseudotype-like virion structure.";
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                            Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                        854 AA
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577 RILAVERYLKDQQLLGIWGCSGKLIC 602
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es 26; Conservative
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Pfam; PF00517; GP41; 1.
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                                                                                                                                                                                                                                                      Envelope glycoprotein.
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Gaps

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Length Indels

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Vidal N., Peeters N., Mulanga-Kabeya C., Nzilambi N., Robertson D., Ilunga W., Sema H., Tshimanga-Kabeya C., Nzilambi N., Robertson D., Ilunga W., Sema H., Tshimanga-Kabeya C., Delaporte E.; Ilunga W., Sema H., Tshimanga K., Bongo B., Delaporte E.; Unprecedented degree of human immunodeficiency virus Type 1 (HIV-1) group M genetic diversity in the Democratic Republic of Congo suggests that the HIV-1 pandemic originated in Central Africa.", J. Virol. 74:10498-10507(2000).

EMBL, AJ401041; CAC15049.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000328; Env GP41.
                                                                                                                 Pfam; PF00516; GP120; 1.
Pfam; PF00516; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 854 AA; 96885 WW; 0808F3AED27C693B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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           GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein gp120.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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; Pred. No. 1e-12;
0; Mismatches 0;
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100.0%; Pred. No. 1e-12;
ive 0; Mismatches 0;
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STRAIN-J 97DC.KTB147;
MEDLINE-Z0499072; PubMed=11044094;
                                                                                                                                                                                                                                                                         100.08;
                                                                                                                                                                                                                                                                                                L Similarity 100.0%;
26; Conservative 0
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Q78705;
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The decular clone.

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                          Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
"Recovery of virtually full-length HIV-1 provirus of diverse subtypes
from primary virus cultures using the polymerase chain reaction.";
Virology 213:80-86(1995).
                                                                                                                                                                                                                                                                                    Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
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Fang H., Pincus S.H.,
"Spontaneous activation of human immunodeficiency virus type 1 in an
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Pred. No. 1e-12;
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF070521; ARC28452.1; -..
PIR; A53591; A53591.
PIR; A53591; A53591.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
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A -> S (IN REF. 2).
G -> D (IN REF. 2).
; FF2264B3841D1220 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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MEDLINE=86281827; PubMed=3016298;
Formion
MEDLINE=96036482; PubMed=7483282;
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Best Local Similarity 100.0%;
Matches 26; Conservative 0
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=99098984; PubMed=9882298;
Cayabyab M., Karlseon G.B., Etemad-Moghadam B.A., Hofmann W.,
Steenbeke T., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,
Sodroski J.G.;
"Changes in human immunodeficiency virus type 1 envelope glycoproteins
responsible for the pathogenicity of a multiply passaged simian-human
immunodeficiency virus (SHIV-HXBc2).";
J. Virol. 73:976-984(1999).
                                                                                                                                                                                               Cloyd M.W., Moore B.E.; "Spectrum of Biological Properties of Human Immunodeficiency Virus (HIV-1) Isolates.";
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NCE 856 AA, 97396 MW, FE3E784C423C108C CRC64;
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GO: GO:0016021; C:integral to membrane; IEA.
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:00190319; F:structural molecule activity; IEA.
InterPro; IPR000777; GP120.
Pfam; PF00515; GP120; 1.
Pfam; PF00517; GP41; 1.
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                       Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
VicBl_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentívirus.
NCBI_TaxID=57667;
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MEDLINE=90101366; PubMed=1688473;
                                                                                                                                                                                                                                                       Virology 174:103-116(1990)
                                                                                                                                                                                                                                                                                                                                                            EMBL, D86069; BAA13003.1;
PIR, A53591; A53591.
PIR, S13288; S13288.
PDB; 1F23; 20-JUN-01.
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Matches 26; Conserv
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                               SEQUENCE FROM N.A.
MEDLINE=96013815; PubMed=7474132;
Duensing T.D., Fang H., Dorward D.W., Pincus S.H.;
"Processing of the envelope glycoprotein gpls60 in immunotoxin-resistant cell lines chronically infected with human immunodeficiency
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Libery P., Salemi M., Wang B., Saksena N.K., Vandamme A.M.;
Lemey P., Salemi M., Wang B., Saksena N.K., Vandamme A.M.;
Lemey P., Salemi M., Wang B., Saksena II HIV.
Implications on Dating Strategies in HIV Molecular Phylogenies.";
Submitted (ANG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF538302; AAN64079.1; --
GO; GO:0019031; C:virtal envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000777; GPIZO.
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SEQUENCE 854 AA; 97199 MW; 5B9512216533R256 CRC64;
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Pfam; PF00517; GP41; 1.
SEQUENCE 855 AA; 97180 MW; 81887BBFAD516F27 CRC64;
                                                                                                                                                                                                            GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR00077; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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100.0%; Pred. No. 1e-12;
iive 0; Mismatches 0;
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Pred. No. 1e-12;
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                                                                                                                        virus type 1.";
J. Virol. 69:7122-7131(1995).
EMBL, 142371; AAA96326.1; -.
PIR; A53591; A55591.
PIR; S13288; S13288.
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Matches 26; Conserv
NCBI_TaxID=11676;
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STRAIN=ACH168.10;

Lacasse R.A., Follis K.E., Moudgil T., Trahey M., Binley J.M.,

Lacasse R.A., Follis K.E., Moudgil T., Trahey M., Binley J.M.,

R. "Coreceptor utilization by human immunodeficiency virus type 1 is not

The string of determinant of neutralization sensitivity.";

J. Virol. 0:0-0(1997).

R. EMBL, AF03533; AAB9954.1; -.

R. GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid, IEA.

GO; GO:0019031; C:viral capsid, IEA.

RO; GO:0005198; F:structural molecule activity; IEA.

R. InterPro; IPR000328; Env GP41.
                                                                                                                                                                        STRAIN=ACH168.10;
MEDLINE=55074890; PubMed=7983734;
MEDLINE=55074890; PubMed=7983734;
Wrin T., Loh T.P., Vennari J.C., Schuitemaker H., Nunberg J.H.;
"Adaptation to persistent growth in the H9 cell line renders a primary isolate of human immunodeficiency virus type 1 sensitive to neutralization by vaccine sera.";
J. Virol. 69:39-48(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=168C;
MEDLINE=95074890; PubMed=7983734;
MEDLINE=95074890; PubMed=7983734;
Mrin T., Loh T.P., Vennari J.C., Schuitemaker H., Nunberg J.H.;
"Adaptation to persistent growth in the H9 cell line renders a primary isolate of human immunodeficiency virus type I sensitive to neutralization by vaccine sera.";
J. Virol. 69:39-48(1995).
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Pfam; PF00517; GP41; 1.
AlDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 857 AA; 97370 MW; 3EB213BD2DCD485D CRC64;
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               08, Last sequence update) 24, Last annotation update)
                                                                                  Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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01-JUN-2003 (TrEMBLrel.
Envelope glycoprotein.
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Cloyd M.W., Moore B.B.;
"Spectrum of Biological Properties of Human Immunodeficiency Virus (HIV-1) Isolates.";
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SEQUENCE 856 AA; 97151 MW; C50BE0388FB73659 CRC64;
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NCE 856 AA; 97287 MW; 238042A234C5668S CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A lwatani Y.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; D86608; BAA12995.1;
PPIR, 543591, A55591.
PPIR, 543591, A55591.
PPIR, 513288; 513288.
R PIR; 513288; Co-UNW-01.
R GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019021; C:integral to membrane; IEA.
GO; GO:0019031; C:integral to membrane; IEA.
GO; GO:0019031; C:integral to membrane; IEA.
R O; GO:0019031; C:integral to membrane; IEA.
GO; GO:0019031; C:integral to membrane; IEA.
R InterPro; IPR000777; GP120.
R Pfam; PF00517; GP120.
R Pfam; PF00517; GP41; 1.
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pred. No. 1e-12;
                                                                                                                                                                                Score 139; DB 15;
Pred. No. 1e-12;
: Mismatches 0;
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100.0%; Pred. No. 10.
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01-NOV-1998 (TrEMBLrel. 08, Created)
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virology 174:103-116(1990).
                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 26; Conservative
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Best Local Similarity 100.0
Matches 26; Conservative
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MEDLINE=95074890; PubMed=7983734; Wrin T., Loh T.P., Vennari J.C., Schuitemaker H., Nunberg J.H.; Wrin T., Loh T.P., Vennari J.C., Schuitemaker H., Nunberg J.H.; Adaptation to persistent growth in the H9 cell line renders a primary isolate of human immunodeficiency virus type I sensitive to neutralization by vaccine sera.";
                                                                                                                                                                                                                                                       Planelles V., Zolla-Pazner S., Vunberg J.H.;

"Coreceptor utilization by human immunodeficiency virus type 1 is not a primary determinant of neutralization sensitivity.";
J. Virol. 0:0-0 (1997).

EMBL; AF035534; A8099955.1; --
GO; GO:0010021; C:integral to membrane; IEA.
GO; GO:0010031; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0010931; C:viral molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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Ald S Res. Hum. Retroviruses 16:139-151(2000).

EMBL; AJ249237; CAB59982.1; -...

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral expedid; IEA.

GO; GO:0019031; C:viral expedid; IEA.

GO; GO:0019031; C:viral molecule activity; IEA.

InterPro; IPR000328; Bru GP41.
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Triques K., Bourgeois A., Vidale N., Mpoudi-Ngole E.,
Mulanga-Kabeya C., Nzilambi N., Torimiro N., Saman E., Delaporte E.,
Peeters M.;
                                                                                                                                                                                                                                                 LaCasse R.A., Follis K.E., Moudgil T., Trahey M., Binley J.M.,
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 857 AA; 97508 MW; D0451S0ACBDCOBF6 CRC64;
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AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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1C81CD10C59379A0 CRC64;
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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100.0%; Pred. No. 1e-12;
ive 0; Mismatches 0;
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                                                                                                                                     J. Virol. 69:39-48(1995)
[2]
SEQUENCE FROM N.A.
STRAIN=168C;
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Best Local Similarity
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01-JUN-2003
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                                                                                                                                                                                                 Gaps
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Pfam, PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 857 AA, 97505 WW, 039E68247BDC005A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neutralization by vaccine sera.";
J. Virol. 69:39-48(1995).
EMBL; U15032; AA464970.1;
EMBL; U15030; AAA64868.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                     Query Match 100.0%; Score 139; DB 15; Best Local Similarity 100.0%; Pred. No. 1e-12; Matches 26; Conservative 0; Mismatches 0;
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; Pred. No. 1e-12;
0; Mismatches 0;
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MEDLINE=95074890; PubMed=7983734;
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InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
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Best Local Similarity 100.0%;
Matches 26; Conservative 0
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SEQUENCE 860 AA
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01-OCT-2003
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MEDLINE=9903935; PubMed=9824329;
OGITICNE=9903935; PubMed=9824329;
OGITICNE R.B., Workman C., Laukkanen T., McCutchan F.E., Deacon N.J.;
"A novel subtype A/G/J recombinant full-length HIV type 1 genome from
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                               Carr J.K., Laukkanen T., Salminen M.O., Albert J., Alaeus A., Kim Sanders-Buell E., Birx D.L., McCutchan F.E., "Characterization of subtype A HIV-1 from Africa by full genome
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                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 859 AA; 96945 MW; B49458013BA96EB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 139; DB 15; Length 859; 100.0%; Pred. No. 1e-12; ive 0; Mismatches 0; Indels 0;
                   Indels
                                                                                                                                                                                                                                                                                                sequencing.";
AIDS 13:1819-1826(1999).
EMBL; AF065672; AAD13364.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:00019189; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
                                                                                                                                  01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                        Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
1e-12;
0;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                859 AA
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   100.0%; Preα. ....
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                                                          580 RILAVERYLKDOOLLGIWGCSGKLIC 605
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                                       1 RILAVERYLKDQQLLGIWGCSGKLIC
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                                                                                                                PRT;
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                                                                                                                                                                                                                                             STRAIN=SE6594;
MEDLINE=99441797; PubMed=10513639;
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Best Local Similarity 100.0
Matches 26; Conservative
     Best Local Similarity 100.
Matches 26; Conservative
                                                                                                               PRELIMINARY;
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                                                                                                                                                                   Envelope glycoprotein.
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                                                                                                                                                                                                              NCBI_TaxID=11676;
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                                                                                                              Q9YUZ4
Q9YUZ4;
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                                                                                           RESULT 57
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Delgado E., Thomson M.M., Villahermosa M.L., Sierra M., Ocampo A.,
Miralles C., Rodriguez-Perez R., Diz-Aren J., Ojea-de-Castro R.,
Losada E., Cuevas M.T., Vazquez de Parga E., Carmona R.,
Perez Alvarez L., Medrano L., Cuevas L., Taboada J.A., Najera R.,
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                                                                                                                                                                                                                                                  Coat protein; Glycoprotein; Polyprotein; Transmembrane.
NCE 859 AA; 96504 MW; 41BB25F110C38E0C CRC64;
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF064699; AAD03314.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:integral to membrane; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000328; F:structural molecule activity; IEA.
InterPro; IPR000777; GPI20.
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Tatsumi M., Matsuda M.;
Tatsumi M., Cones of HIV-1 subtype A.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB098332; BAC77753.1; -
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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; Pred. No. 1e-12;
0; Mismatches 0;
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Pred. No. 1e-12;
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Best Local Similarity 100.0%;
Matches 26; Conservative (
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                                                                                                                                                                                                                           Pfam; PF00517; GP41; 1.
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Burger H.;

"Complete Plasma HIV-1 Sequence: Spl-Promoter Deletion Can Lead to Non-Progressive Infection."

Non-Progressive Infection.";

Submitted (SEP-196) to the EMBL/GenBank/DDBJ databases.

EMBL; U69589; AAD1091s.1;

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral envelope; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0019031; C:viral molecule activity; IEA.

InterPro; IPR000328; Bry GP120.
                                                                                          SEQUENCE FROM N.A.
Fang G., Weiser B., Chappey C., Visosky A., Townsend L., Wang Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane. SEQUENCE 864 AA; 98272 MW; C29EE033EE9D2D99 CRC64;
                        Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 139; DB 15;
100.0%; Pred. No. 1e-12;
ive 0; Mismatches 0;
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    Human immunodeficiency virus 1.
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InterPro; IPR000777; GP120.
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Best Local Similarity 100.
Matches 26; Conservative
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Pfam; PF00517; GP41; 1.
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                                            NCBI_TaxID=11676;
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SEQUENCE 864 AA
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                                                                                                                                    STRAIN=X665;

Delgado E., Thomson M.M., Villahermosa M.L., Sierra M., Ocampo A.,
Delgado E., Thomson M.M., Villahermosa M.L., Sierra M., Ocampo A.,
Miralles C., Rodriguez-Perez R., Diz-Aren J., Ojea-de-Castro R.,
Loadda E., Cuevas M.T., Vacquez de Parga B., Carmona R.,
A Perez Alvarez L., Medrano L., Cuevas L., Taboada J.A., Najera R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF450096; AAL47033.1; --
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0019028; C:viral capsid; IEA.
R GO; GO:0019028; F:viral envelope; IEA.
R GO; GO:001919; F:structural molecule activity; IEA.
R InterPro; IPR000328; Env GP41.
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0
"Identification of a newly characterized HIV-1 BG intersubtype Circulating Recombinant Form in Galicia, Spain, exhibiting a pseudotype-11ke virion structure.";

O. Acquir. Immune Defic. Syndr. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 862;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coat protein, Glycoprotein, Polyprotein, Transmembrane.
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Tatsum M., Matsuda M.;
"Infectious DNA clones of HIV-1 subtype A.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB098333; BAC77762.1; -.
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01-OcT-2003 (TrEMBLrel. 25, Last sequence update)
01-OcT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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NCBI_TaxID=11676;
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Pred. No. 1e-12;
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100.0%; Score 139; Dest Local Similarity 100.0%; Pred. No. 1e-Matches 26; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           PF00516; GP120; 1.
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                                                                                                                   SEQUENCE FROM N.A.
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SEQUENCE 862 AA
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Q9YP39
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STRAIN-US4;
STRAIN-US4;
Hierholzer J., Montano S., Hoelscher M., Negrete M.,
Hierholzer M., Avila M., Gomez Carrillo M., Russi J., Vinoles J.
Alava A., Acosta M., Giannella A., Andrade R., Sanchez J.L.,
Carrion G., Sanchez J., Robb M., Birx D., McCutchan F.;
"Molecular Epidemiology of HIV type 1 in Ecuador, Peru, Bolivia,
Uruguay and Argentian ",
AIDS Res. Hum. Retroviruses 0:0-0(2003).
EMBL; AV173955; AAO63221.1;
GO: GO:0019031; C:Viral envelope; IEA.
GO: GO:0019031; C:Viral envelope; IEA.
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                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                        Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Length 868;

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Gorry P.R., Taylor J., Holm G., Mehle A., Morgan T., Cayabyab M.,

R Farzan M., Wang H., Bell J.E., Kunstman K.J., Moore J.P.,

R Parzan M., Gabuzda D.;

Rolinsky S.M., Gabuzda D.;

"Increased CCR5 affinity and reduced CCR5/CD4 dependence of a
"Increased CCR5 affinity and reduced CCR5/CD4 dependence of a
"Increased CCR5 affinity and reduced CCR5/CD4 dependence of a
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GOLY P.R., Taylor J., Holm G., Mehle A., Morgan T., Cayabyab M.,
Farzan M., Wang H., Bell J.E., Kunstman K.J., Moore J.P.,
Wolinsky S.M., Gabudza D.;
"Increased CCR5 affainty and reduced CCR5/CD4 dependence of a
neurovirulent primary human immunodeficiency virus type 1 isolate.";
J. Virol. 0:0-0(2002).

EMBL; AF491742; AAM09795.1; -.
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 870 AA; 99067 MW; 067C44F6526160DF CRC64;
                5EFDFE3B73746F13 CRC64;
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
                                                           DB 15;
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100.0%; Score 139; DB 15
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches C
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                98621 MW;
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             868 AA;
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01-JUN-2002 (
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MEDLINE=99236722; PubMed=10221533;
Quinnan G.V. Jr., Zhang P.E., Fu D.W., Dong M., Alter H.J.;
Guinnan G.V. Jr., Zhang P.E., Fu D.W., pool of H.V. type I envelope protein associated with a broadly reactive neutralizing antibody response.";
AIDS Res. Hum. Retroviruses 15:561-570(1999).
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A RIGOZIUS-22375625; PubMed=12487816;

A Rigozi G., Kiwanuka N., Sewankambo N., Wabwire F., Kim B.,

A Rigozi G., Kiwanuka N., Phillips J.B., Meehen M., Lutalo T.,

Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L.,

A McCutchan F.E.;

T. Among 46 Near Full Length HIV Type I Genome Sequences from Rakai

District, Uganda, Subtype D and AD Recombinants Predominate.";

A IDS Res. Hum. Retrovitues 18:1281-1290(2002).

E RMBL, AF484691, AAN73652.1;

GO: GO:0019031; C:viral envelope; IEA.

GO: GO:0019031; C:viral molecule activity; IEA.

R InterPro: IPR000328; Env GP41.

R InterPro: JPR001577; GP120.

R Pfam; PF00516; GP120; 1.
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NCE 866 AA; 98081 MW; 44D9329789833122 CRC64;
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Quinnan G.V. Jr., Zhang P.F., Fu D.W., Dong M., Alter H.J.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

BMBL, AF128126; AAD40637.2; -
GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:00051991; F:structural molecule activity; IEA.

InterPro; IPR000328; ENV GP41.

InterPro; IPR000777; GP120.
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                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                          Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBL_TaxID=11676;
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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100.0%; Pred. No. 1e-12;
1ve 0; Mismatches 0;
                           866 AA
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1es 26; Conservative
                       PRELIMINARY;
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Pfam; PF00517; GP41; 1.
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              "Detection of HIV-1 RNA in two consecutive blood donations screened
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                                negative for HIV-antibody.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, Y11839; CAA72537.1; -.
GO; GO:0016021; C:integral; to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPror; IPR000328; Env_GP41.
Transmembrane.
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109 AA; 12705 MW; CDE3D9FES574175E CRC64;
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EMBL; AF465196; AAL66706.1, -

EMBL; AF465196; AL66706.1, -

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:005198; F:etructural molecule activity; IEA.

InterPro: IPR00517; GP41; 1.

PF00517; GP41; 1.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein gp41 (Fragment).
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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NCBL_TaxID=11676;
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MEDLINE=21602569; PubMed=11739704;
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T Virol. 76:397-405(2002)
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nes 25; Conservative
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Q8UQW2
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Beteves A., Parreira R., Venenno T., Franco M., Piedade J.,
Germano de Sousa J., Canas-Ferreira W.;
"Genetic diversity of HIV-1 spreding among intravenous drug users in
Lisbon, Portugal.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ429040; CAD23676.1; --
EMBL; GA:

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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41: 1.
                                                                                                                                                                                                                                                                                                                  DB 15; Length 870;
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Pred. No. 1.5e-13;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                 Score 139; DB 15; Lengard Pred. No. 1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 AA; 11165 MW; B59B27115A79E800 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Transmembrane glycoprotein gp41 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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100.0%;
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Best Local Similarity 96.2%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                         Query Match 100.0
Best Local Similarity 100.0
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MP109;
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Q8AEX3
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RESULT 73

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STRAIN=96USNG46;
Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ellenberger D., Sullivan P.S., Dorn J., Schable C., Spira T.J., Polks T.M., Lal R.B.; Viral and Immunologic Examination of HIV-1-infected Persistently Seronegative (HIPS) Persons."; J. Infect. Dis. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.3%; Score 138; DB 15; Length 117; 96.2%; Pred. No. 1.8e-13; Live 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 117
117 AA; 13920 MW; 39BD6AAE4FAD37AA CRC64;
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                                                      (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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                                                                                                                  Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
Vill_TaxID=11676;
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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                           117 AA
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                           PRT;
                                                                                                        Envelope glycoprotein (Fragment).
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
                       PRELIMINARY;
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SEQUENCE FROM N.A.
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les 25; Conserv
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                                                      01-MAY-1999
01-MAY-1999
01-JUN-2003
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Q9YRS4;
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Q900N0
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Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
StrAIN=SGUSNGIS;
Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
Jones J., Ward J.;
"Surveillance of Central African Nationals living in the United States
reveals multiple subtypes of HIV-1 Group M and Group O.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF096334; AAD0440901; --
GO; GO:0019031; C:integral to membrane; IEA.
GO; GO:0019031; C:integral to membrane; IEA.
GO; GO:00190319; C:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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                                                                                          Ellenberger D., Sullivan P.S., Dorn J., Schable C., Spira T.J., Folks T.M., Lal R.B.;
"Viral and Immunologic Examination of HIV-1-infected Persistently Seronegative (HIPS) Persons ";
J. Infect. Dis. 0:0-0(1999).
EMBL; AF157468; AAD45888.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001598; F:structural molecule activity; IEA.
InterPro; IPR000328; Env.GP41: 1.
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1 Similarity 96.2%; Pred. No. 1.8e-13;
25; Conservative 1; Mismatches من تبیکری
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117 117
117 AA: 14011 MW; 9A71687C21470E60 CRC64;
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Human immunodeficiency virus 1.
Viruses, Retroid viruses, Retroviridae, Lentivirus.
VGBI_TaxID=11676;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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NCBI_TaxID=11676;
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                                                                FROM N.A.
                                                                            STRAIN=96USHIPS7;
                                                                                                                                                                                                                                                                               Transmembrane
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SEQUENCE FROM N.A.
STRAIN=140.330;
Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
                                                                                                                                                                                               Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 117;
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117 117
117 AA; 13864 MW; C8F2F6CBC0A5437F CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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NCBI_TaxID=11676,
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                          Query Match 99.3%; Score 138; DB 15; Best Local Similarity 96.2%; Pred. No. 1.8e-13; Matches 25; Conservative 1; Mismatches 0;
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Pred. No. 1.8e-13;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA
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                         InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
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Best Local Similarity 96.2%;
Matches 25; Conservative
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Q9WM72
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Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M., Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M., Jones J., Ward J.;
Jones J., Ward J.;
Surveillance of Central African Nationals living in the United States reveals multiple subtypes of HIV-1 Group M and Group O.";
Submitted (CCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR096340; AAD04415.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0015031; C:viral envelope; IEA.
GO; GO:001598; F:structural molecule activity; IEA.
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                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=135.544;
Brennan C.R., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
Phillips J.R., Kataaha P.K., Jackson J.B., Devare S.G.,
"Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
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                                                 Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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NCBI_TaxID=11676;
Pred. No. 1.8e-13;
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            96.2%; Preα. ....
tive 1; Mismatches
                                                                                                                            23 RVLAVERYLKDQQLLGIWGCSGKLIC 48
                                                                                               1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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                                              25; Conservative
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                  Best Local Similarity
Matches 25; Conserv
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Q9YZ04
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Q9YRS6

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Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                   NCBI_TaxID=11676;
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Q9YRS2
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C STRAIN=SOUGHIESS;
A Folks T.M., Lal R.B.;
T "Virtal and Immunologic Examination of HIV-1-infected Persistently J. Infect. Dis. 0:0-0(1999).

E Seronegative (HIPS) Persons.";
J. Infect. Dis. 0:0-0(1999).

R EMBL, AFLEAT/07, AAD45890.1;
R GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:integral to membrane; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R Fiam; PF00517; GP41; I.
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Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G., "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
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                                                              Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF006868; AAD01312.1; -. Genbrane; IEA. GO; GO:0016021; C:inregaral to membrane; IEA. GO; GO:0019031; C:inregaral to membrane; IEA. GO; GO:005198; F:structural molecule activity; IEA. InterPro; IRR000328; Env GP41.
                                                                                                                                                                                                                                                             117 117 117 117 117 423078A5169EB536 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein gp41 (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                         25; Conservative
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Q9YZ01;
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Q9QQN3
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Q9YZ01
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Surveillance of Central African Nationals living in the United States reveals multiple subtypes of HIV-1 Group M and Group O.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF0963344; AAD04419.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0015031; C:viral envelope; IEA.
InterPro; IPR000328; Env GP41.
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STRAIN-161.287;
STRAIN-161.287;
Brenan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
"Serologic and Phylogenetic Characterization of HIV-1 Subtypes in Uganda.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF006872; AAD01316.1; -
GO; GO:0019031; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; F:structural molecule activity; IEA.
InterPro; IPR000328; ENV. GP41: 1.
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117 AA; 13950 MW; C3C550C19DB602E6 CRC64;
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117 117
117 AA; 14004 MW; 11CA37F5C8C6278F CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Matches 25; Conservative
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STRAIN=96USTG17;
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RESULT 82

01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-UUN-2003 (TrEMBLrel. 24, Last annotation update)

Gp41 (Fragment) ENV.

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PRELIMINARY;
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                                                                               Q7SVI4;
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Q7SVG4
RESULT 84
Q7SVI4
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Q7SVG1
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                                                                                                                                                                                                                                                                                                     STRAIN=204.987;
Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
"Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
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GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0019031; C:viral envelope; IEA.
GO, GO:0005198; F:structural molecule activity; IEA.
InterPro; IRR00328; Env_GP41.
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117 Aa; 13948 MW; 7FA9BE6B7BF8B39E CRC64;
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                                          01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein gp41 domain (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                         Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
  117 AA.
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Matches 25; Conserv
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SEA C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.;
"Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N., Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.; "presence of HTV-2 subtype B in single and HTV-2 subtype A in dual HTV-1/HTV-2 infections in Nigeria."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                          HIV-1/HIV-2 infections in Nigeria.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AY102800; AAM51895.1; -.
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                                       01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein gp41 domain (Fragment).
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Pred. No. 1.8e-13;
                                                                                                                Envelope glycoprotein gp41 domain (Fragment).
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96.2%; Pred. No. ...
1; Mismatches
117 AA
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Best Local Similarity 96.2.
Local Similarity 96.2.
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Matches 25; Conservative
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SEQUENCE FROM N.A.
STRAIN-99NG761;
Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
Zeh C., Agwale S.M., Rubbins R.E., Ddama L., Sani-Gwarco N.,
Zeh C., Poleniazek D., Wambebe C., Folks T.M., Kalish M.L.;
"Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
HIV-1/HIV-2 infections in Nigeria.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX102827; AAM51922.1;
BATCO AMS AM51922.1;
AMS AM51922.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-99NG779;
Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
Zeh C., Agwale S.M., Wambebe C., Folks T.M., Kalish M.L.;
"Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
HIV-1/HIV-2 infections in Nigeria.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX102830; AAM51925.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 99.3%; Score 138; DB 15; Length 117; Best Local Similarity 96.2%; Pred. No. 1.8e-13; Matches 25; Conservative 1; Mismatches 0; Indels (
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                     Viruses; Retroid viruses; Retroviridae; Lentivirus NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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       01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
                                                       Envelope glycoprotein gp41 domain (Fragment).
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01-0CT-2003 (TrEMBLrel. 25, Last annotation u
Envelope glycoprotein gp41 domain (Fragment).
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Ed. C., Agwale S.M., Robbins K.B., Odama L., Sani-Gwarco N.,
Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.;
"Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
HIV-1/HIV-2 infections in Nigeria.";
Submitted (MAY-2002) to Nhe EMBL/GenBank/DDBJ databases.
EMBL; AY102823; AAMS1918.1; -.
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99.3%; Score 138; DB 15; Length 117;
Best Local Similarity 96.2%; Pred. No. 1.8e-13;
Matches 25; Conservative 1; Mismatches 0; Indels
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117 AA; 13960 MW; 9FC5F46458277DDB CRC64;
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117 AA; 14085 MW; 887D3F6DFEEAA6E6 CRC64;
                                                                     01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein gp41 domain (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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01-CCT-2003 (TrEMBLrel. 25, Last annotation up
Envelope glycoprotein gp41 domain (Fragment).
    117 AA
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01-0CT-2003 (TrEMBLrel. 25, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
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01-OCT-2003 (TrEMBLrel. 25, Created)
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RESULT 88 Q7SVF7

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1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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SEQUENCE FROM N.A.
   NCBI_TaxID=11676;
                                     STRAIN=99NG859;
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Q7SVE7
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Q7SVE4
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RRA RRA
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                                                                    STRAIN=99NG77;
Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.,
"Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=99NG782;
Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.;
"Presence of HIV-2 subtype in single and HIV-2 subtype A in dual
HIV-1/HIV-2 infections in Nigeria.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX102832; AAM51927.1; -.
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                                                                                                                                                                                                                99.3%; Score 138; DB 15; Length 117; 96.2%; Pred. No. 1.8e-13; tive 1; Mismatches 0; Indels (
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                                                                                                                  HIV-1/HIV-2 infections in Nigeria.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AY102831; AAM51926.1; -.
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117 AA; 13937 MW; C30B6DFEDF71B169 CRC64;
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117 AA; 14029 MW; 92B245BDB91467C6 CRC64;
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein gp41 domain (Fragment).
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein gp41 domain (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Best Local Similarity 96.2*
Matches 25; Conservative
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SEQUENCE 117 AA;
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SEQUENCE
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Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N., Zeh C., Agwale S.M., Robbins K.E., Odama L., Kalish M.L.; Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.; Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual HIV-1/HIV-2 infections in Nigeria."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.;
"Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
HIV-1/HIV-2 infections in Nigeria.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX102837; AAM51932.1;
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117 AA; 14076 MW; E3B8E5D24354D5B3 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein gp41 domain (Fragment).
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein gp41 domain (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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NCBI_TaxID=11676,
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Pred. No. 1.8e-13;
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Pred. No. 1.8e-13;
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Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P., Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.; Presence of human immunodeficiency virus (HIV) type 1, group M, non-B subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic diversity in the United States.", J. Infect. Dis. 181:470-475 (2000).
                                                                                                                                                                                                                                                                                                       STRAIN-UG;
Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund of Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

BMBL; AR307736, AAL08797.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0015031; C:integral to membrane; IEA.

GO; GO:005198; F:structural molecule activity; IEA.

InterPro; IPR00328; Env. GF41.
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121 AA; 14560 MW; C4601F79660BBC5D CRC64;
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                    (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR00328; Env_GP41.
Pfam; PF00517; GP41; 1.
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                 Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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NCBI_TaxID=11676;
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96.2%; Pred. No. 1.9e-13;
ative 1; Mismatches 0;
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                                                                                                           Envelope glycoprotein (Fragment).
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01-JUN-2003
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STRAIN-99NG901;
Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
Zeh C., Agwale S.M., Robbins K.E., Odama L., Sani-Gwarco N.,
Gboun M.S., Pieniazek D., Wambebe C., Folks T.M., Kalish M.L.;
Presence of HIV-2 subtype B in single and HIV-2 subtype A in dual
HIV-1/HIV-2 infections in Nigeria.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
Envelope protein.

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117

117

SEQUENCE 117 AA; 14021 MW; 771766CAD25F3EE4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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14256 MW; CCCA2AF34D192690 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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RESULT 95 Q9E5R0

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RESULT 96 Q90DJ5 ID Q90DJ! AC Q90DJE

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Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
"Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
diversity in the United States.",
J. Infect. Dis. 181:470-475(2000).
EMBL, AR190967; ARG02239.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:viral envelope; IEA.
GO; GO:0016031; C:viral envelope; IEA.
GO; GO:0005198; P:structural molecule activity; IEA.
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STRAIN=GP4IERRJ03;

Caride E., Hertogg K., Larder B., Dehertogh P., Brindeiro R.,
Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
Calazans A.R., Tanuri A.;
"Genotyping and phenotyping analysis of B and non-B Human
immunodeficiency virus type I subtypes from patients under HAARI.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF165536; AAF08481.1;
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99.3%; Score 138; DB 15; Length 122; 96.2%; Pred. No. 1.9e-13; ive 1; Mismatches 0; Indel8
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                        1 RILAVERYLKDQQLLGIWGCSGKLIC 26
                                                                                          1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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MEDLINE=20134570; PubMed=10669328;
                                                                                                                                                                                                                                                                                 Envelope glycoprotein (Fragment).
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Pfam; PF00517; GP41; 1.
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 Query Match 99.3
Best Local Similarity 96.2
Matches 25; Conservative
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Q9QIW8
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GO: GO: 0016021; C:integral to membrane; IEA.

GO: GO: 0019031; C:viral envelope; IEA.

GO: GO: 0005199; Fstructural molecule activity; IEA.

PERMO CO: 1 PR0000228; Env. GP41.
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122 AA; 14663 MW; AAC57DB097817188 CRC64;
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                                                                                                                                         Last sequence update)
Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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NCBI_TaxID=11676,
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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                                                                                                                         Created)
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                                                                                                                                                                          Envelope glycoprotein (Fragment).
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity 96.24
Matches 25; Conservative
                                                                                     PRELIMINARY;
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122 AA;
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X MEDLINE=X0923,
X MEDLINE=X0923,
X MEDLINE=X0194570; PubMed=10669328;
X MEDLINE=20134570; PubMed=10669328;
X MEDLINE=20134570; PubMed=10669328;
X Meddle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
X Meidle P.J., Ganea C.E., Lal R.B., Holmberg S.D., Ernst J.A.;
X Tresence of human immunodeficiency virus (HIV) type 1, group M, non-B
X Subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
X J. Infect. Dis. 181:470-475(2000).
X J. Infect. Dis. 181:470-475(2000).
X GO:0010911; C:integral to membrane; IEA.
X GO:0005198; F:structural molecule activity; IEA.
X InterPro; JRR000328; Bnv_GP41.
X Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF034053; AAC79305.1, -
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0015031; C:viral envelope; IEA.
GO, GO:005198; F:structural molecule activity; IEA.
InterPro, IPR00328; Env GP41; 1.
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Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
                                                                                                                                                                                                                                                                                                                                                                                        99.3%; Score 138; DB 15; Length 122; 96.2%; Pred. No. 1.9e-13; Live 1; Mismatches 0; Indels (
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99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein immunodominant region (Fragment).
                                                                                                                                                                                                                                                                                                                                                   122 AA; 14753 MW; C3FE4DB1F8B5BCBD CRC64;
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122 AA; 14733 MW; BOO8FE9FF1F36DOC CRC64;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                 SEQUENCE FROM N.A.
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09EAA4;
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Q9EAA4
ID Q9EAA4
AC Q9EAA4
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A Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
A Machado E., de Sa C.-A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
Calazans A.R., Tanuri A.;
"Genotyping and phenotyping analysis of B and non-B Human
immunodeficiency virus type 1 subtypes from patients under HAART.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
BMBL; AR165543; AAR08488.1;
BMBL; AR165543; AR08488.1;
BMSD; GO:0019031; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
RO; GO:0019031; C:viral envelope; IEA.
RO; GO:0005188; F:structural molecule activity; IEA.
RITEETPO; IPR00317; GP41:
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122 AA; 14708 MW; 4FF31B6E9075EE55 CRC64;
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122 AA; 14733 MW; E2049BD5BAA9A6F0 CRC64;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:efructural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
Transmembrane.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UUN-2003 (TrEWBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Best Local Similarity 96,2%
Matches 25, Conservative
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Q9EA81;
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RESULT 103 Q9EA81

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MEDLINE=20346416; PubMed=10890362;
Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A., Bagged J., Lal R., Pieniazek D.;
Baggs J., Lal R., Pieniazek D.;
"Evidence for a high frequency of HIV-1 subtype F infections among heterosexual population in Buenos Aries, Argentina.";
AIDS Res Hum. Retroviruses 16:1007-1014(2000).
EMBL; AF220701; AAF76820.1;
GO; GO:0019031; C:inregral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41: 1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                   Viruses; Retroid viruses; Retroviridae; Lentivirus (VCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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Pred. No. 1.9e-13;
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96.2%; Pred. No. 1...
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Q90DQ9
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STRAIN=BX157;
STRAIN=BX157;
WEDLINE=20134870; PubMed=10669328;
WEDLINE=20134870; PubMed=10669328;
WEDLINE=20134870; PubMed=10669328;
WEDLINE=20134870; PubMed=10669328;
Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
Presence of human immunodeficiency virus (HIV) type 1, group M. non-B subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic diversity in the United States.";
J. Infect. Dis. 181:470-475(2000)
SMUL, ST190948; AGOS310.1;
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral molecule activity; IEA.
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"Genotyping and phenotyping analysis of B and non-B Human immunodeficiency virus type I subtypes from patients under HAART.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AR165544, AAF08489.1;
GO: 0010011; C:integral to membrane; IEA.
GO: GO: 0010011; C:viral envelope; IEA.
GO: GO: 0010011; C:viral envelope; IEA.
HIREPPO: IRPRO00128; Estructural molecule activity; IEA.
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122 AA; 14805 MW; D9C7A2283538108B CRC64;
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122 Aa; 14716 MW; CB39CE85DADE28FE CRC64;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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nes 25; Conservative
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GO, GO:001051; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; E:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41; 1.
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Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
Biryalwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
"Similar distribution and continued predominance of HIV-1 subtypes A
and D infections in Uganda.";
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                                                       99.3%; Score 138; DB 15; Length 122; 96.2%; Pred. No. 1.9e-13; 1.1ve 1; Mismatches 0; Indels (
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99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels
                   122 122
122 AA; 14917 MW; 69477A001A80725D CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEWBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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SEQUENCE FROM N.A.
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EMBL, AF307677; AAL08738.1; ---
GO, GO:0019031; C:integral to membrane; IEA.

GO, GO:0019031; C:viral envelope; IEA.

GO; GO:0019031; C:viral molecule activity; IEA.

HinterPro; IPR000328; Env_GF41.
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Local Similarity 96.2%; Pred. No. 1.9e-13;
es 25; Conservative 1; Mismatches 0; Indels (
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF307656; AAL08717.1; -. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0019031; C:viral envelope; IEA. GO; GO:0005198; F:structural molecule activity; IEA. InterPro; IPR000328; Env GP41.
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122 AA; 14713 MW; A6117281CEA10231 CRC64;
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14678 MW; 4C407CA763CC33F0 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Best Local Similarity 96.29
Matches 25, Conservative
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                                                                                MEDINE=20134570; PubMed=10669328; Medide P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P., Medide P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P., Medide P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P., Medide P.J., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A., Presence of human immunodeficiency virus (HIV) type 1, group M, non-B subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic diversity in the United States."; J. Infect. Dis. 181:470-475(2000).
J. Infect. Dis. 181:470-475(2000).
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001031; C:viral envelope; IEA.
GO; GO:0005198; P:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
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GO, GO:001901; C:integral to membrane; IEA.

GO, GO:0019031; C:viral envelope; IEA.

GO, GO:0051939; F:structural molecule activity; IEA.

InterPro; IPR000128; Env_GP41: 1.
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99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels
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122 122 123 NW; 040891ADC152BEE4 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
VICB_TaxID=11676;
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RESULT 114

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Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
"Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
diversity in the United States.";
J. Infect. bis. 181:470-475(2000).
EMBL; AF190950; AAG02312.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR307720; AAL08781.1;
GO; GO: 0016021; C.integral to membrane; IEA.
GO; GO: 0015031; C.integral to membrane; IEA.
GO; GO: 0015098; F: Structural molecule activity; IEA.
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122 122
122 AA; 14603 MW; 0937A2095F3DEFDE CRC64;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                  Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
Mal TaxID=11676;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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96.2%; Pred. No. 1.9e-13;
tive 1; Mismatches 0;
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Pfam; PF00517; GP41; 1.
Transmembrane.
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A Gamal L., Saekhou A., Zeh C., Edubio A., A Mydulo W., Robbins K.E., Odama L., Saekhou A., Zeh C., Edubio A., A Mydulo W.M., Sani-Gawazo M., Gboun M.F., Gao F., Reitz M., Hone D., Folks T.M., Pieniazek D., Wambebe C., Kalish M.L.; Hone D., Folks T.M., Pieniazek D., Wambebe C., Kalish M.L.; Rapid Human Immunodeficiency Virus Type I Subtyping."; T. Rapid Human Immunodeficiency Virus Type I Subtyping."; J. Clin. Microbiol. 39:2110-2114(2001).

R ROJ GO:0016021; C:integral to membrane; IEA.

R GO: GO:0016021; C:integral to membrane; IEA.

GO: GO:0016031; C:viral envelope; IEA.

R GO: GO:001631; C:viral envelope; IEA.

R Pian; PRO0517; GP41; 1.
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STRAIN=GP41ERRJ13;
Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
                                                                                                                         122 AA; 14580 MW; 1D2451530391744E CRC64;
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122 AA; 14701 MW; 6A9C866990E66F1E CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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Pred. No. 1.9e-13;
1; Mismatches 0;
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96.2%; Pred. No. 1.9e-13;
tive 1; Mismatches 0;
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Matches 25, Conservative
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                 Pfam; PF00517; GP41; 1.
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Best Local Similarity
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NCBI_TaxID=11676;
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STRAIN-GP41ERRJ08;
Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
Calazans A.R., Tanuri A.;
"Genotyping and phenotyping analysis of B and non-B Human
immunodeficiency virus type I subtypes from patients under HAART.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and D infections in Uganda.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF307657; AAL087198.1;
GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IRR000328; Env GP41; 1.
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VGBI_TaxID=11676;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0013031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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     1; Mismatches
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  25; Conservative
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Matches
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Q9QIW3
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Downing R., Pieniazek D., Hu D.J., Biryahwaho B., Fridlund C., Rayfield M.A., Sempala S.D., Lal R.B.; "Genetic characterization and phylogenetic analysis of HIV-1 subtype C
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Agwale S.M., Robbins K.E., Odama L., Saekhou A., Zeh C., Edubio A., Adwale S.M., Robbins K.E., Odama L., Gao F., Reitz M., Hone D., Nioku O.M., Sani-Gwarzon N., Gao F., Reitz M., Hone D., Folks T.M., Pieniazek D., Wambebe C., Kalish M.L.;
Tokelopment of an env gp41-Based Heteroduplex Mobility Assay for Rapid Human Immunodeficiency Virus Type 1 Subtyping.";
J. Clin. Microbiol. 39:2110-2114(2001).
REMBL, AF343905; AAK66172.1;
RO; GO:0016021; C:integral to membrane; IEA.
RO; GO:0019031; C:viral envelope; IEA.
RO; GO:0019031; C:viral envelope; IEA.
RO; GO:0005198; F:structural molecule activity; IEA.
RICHERPO; IPR000328; Env GF41.
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122 AA; 14824 MW; 33645F96145A7B07 CRC64;
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AIDS Res. Hum. Retroviruses 16:815-819(2000).
EMBL, AF206045; AAF82001.1; --
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env. GP41.
        Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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NCBI_TaxID=11676;
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MEDLINE=20284721; PubMed=10826488;
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Best Local Similarity 96.29
Matches 25; Conservative
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Best Local Similarity 96.2
Matches 25; Conservative
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SEQUENCE FROM N.A.
                                                                                                               SEQUENCE FROM N.A.
                                                            NCBI_TaxID=11676;
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Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A., Calazans A.R., Tanuri A.;
Calazans A.R., Tanuri A.;
"Genotyping and phenotyping analysis of B and non-B Human immunodeficiency virus type I subtypes from patients under HAART.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
GO, GO:0016021, Cintegral to membrane; IEA.
GO, GO:0019031, Cintegral to membrane; IEA.
GO; GO:0019031, Civiral envelope; IEA.
GO; GO:0051998; Fstructural molecule activity; IEA.
PPEMP, PPEMP, GP41; 1.
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122 AA; 14847 MW; 4E202AEC6B404A06 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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les 25; Conservative
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Matches 25; Conservative
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Query Match
Best Local Similarity 96.2%;
Matches 25; Conservative
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SEQUENCE FROM N.A.
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01-JUN-2003
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Q90DP5;
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STRAIN=GP91ERRJ14;
STRAIN=GP91ERRJ14;
A Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
A Calazans A.R., Tanuri A.;
Genotyping and phenotyping analysis of B and non-B Human immunodeficiency virus type I subtypes from patients under HAART.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBU databases.
B MBL; AF165547; AAF08492.1;
CG): GO:0016021; C:integral to membrane; IEA.
R GO: GO:0016021; C:integral to membrane; IEA.
R GO: GO:0015031; C:viral envelope; IEA.
R GO: GO:0015031; C:viral envelope; IEA.
R GO: GO:00517; GP41; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Diffections in Uganda.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF307695, AAL08756.1;
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0019031; C:viral envelope; IEA.
GO, GO:005198; F:structural molecule activity; IEA.
Frank, PF00517; GP41; 1.
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122 AA; 14728 MW; EEF439193281EDFE CRC64;
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                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
Vibl_TaxID=11676;
                                                                     122 AA.
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Best Local Similarity 96.2%
Matches 25, Conservative
                                                               PRELIMINARY;
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01-DEC-2001
01-DEC-2001
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        RESULT 123
Q90DN6
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Q9QIV7
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STRAIN=UG;
STRAIN=UG;
Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
"Similar distribution and continued predominance of HIV-1 subtypes A and D infections in Uganda.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307686; AAL08747.1, ...
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:00161981; C:irral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR00512; GP41:
   Gaps
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BMB1, AR307651, AAL08712.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral anvelope; IEA.

GO; GO:0019031; C:viral molecule activity; IEA.
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122 AA; 14688 MW; EDAZA13E7C140E32 CRC64;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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Gaps

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High D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C., Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.; "Similar distribution and continued predominance of HIV-1 subtypes A and D infections in Uganda."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

BMBL, AP307691; AL08752.1; GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:integral to membrane; IEA.

FOR GO:0019031; C:integral to membrane; IEA.

FOR GO:0019031; C:integral to membrane; IEA.

FOR GO:00151981; I...

FOR GO:00151981; I...

PFam; PF(0517; GP41; 1.
   Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
                                                                                                                                                                                                                                        Length 122;
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Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels
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                        "HIV-1 subtypes among blood donors from Rio de Janeiro, Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases. BMBL; AR034066; ARC79318.1; -. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0019031; C:viral envelope; IEA. GO; GO:0019198; F:structural molecule activity; IEA. InterPro; IRR000328; Env. GP41.
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122 122
122 AA; 14718 MW; 97207DA663C5007B CRC64;
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122 AA; 14759 MW; 26EB219834EBAE64 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
VCBI_TaxID=11676;
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Pred. No. 1.9e-13;
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96.2%; Pred. No. ...
1; Mismatches
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tes 25; Conservative
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                                                                                                                                                        Transmembrane.
NON TER 122
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                  Rayfield M.;
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Q90DP0
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Baggs J., Lal R., Pieniazek D.;
Baggs J., Lal R., Pieniazek D.;
Evidence for a high frequency of HIV-1 subtype F infections among heterosexual population in Buenos Aries, Argentina.";
ALDS Res. Hum. Retroviruses 16:1007-1014(2000).
EMBL; AP220727; AAF76846.1;
GO; GO:0016021; Caintegral to membrane; IEA.
GO; GO:0019031; Caintegral to membrane; IEA.
GO; GO:0051931; Caintegral molecule activity; IEA.
InterPro; IPR000328; Enrectural molecule activity; IEA.
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Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
                                                                                                        Match 99.3%; Score 138; DB 15; Length 122; Local Similarity 96.2%; Pred. No. 1.9e-13; es 25; Conservative 1; Mismatches 0; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MIN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein immunodominant region (Fragment).
                                                           122 122
122 AA; 14783 MW; BC2E81D16DFEAADF CRC64;
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122 122
122 AA; 14753 MW; 88DF5986C148B527 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
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Q9YXN7
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STRAIN=MOZ36;
MEDLINE=20284721; PubWed=10826488;
MEDLINE=20284721; PubWed=10826488;
MEDLINE=20284721; PubWed=10826488;
Bowning R., Pieniazek D., Hu D.J., Biryahwaho B., Fridlund C.,
Rayfield M.A., Sempala S.D., Lal R.B.;
"Genetic characterization and phylogenetic analysis of HIV-1 subtype C from Uganda.",
ALDS Res. Hum. Retroviruses 16:815-819 (2000).
EMBL; AF206054; AAF82010.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:00160319; C:integral to membrane; IEA.
GO; GO:001598; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
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EMBL, AF034069; AAC79321.1; "Golfo21; Cintegral to membrane; IEA.

GO, GO:0010931; C:viral envelope; IEA.

GO, GO:0010931; C:viral envelope; IEA.

InterPro; IRR00328; Encuctural molecule activity; IEA.

Pfam; PF00517; GP41; 1.
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122 122
122 AA; 14771 MW; BCA91CA7B60ED207 CRC64;
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01-MAX-1999 (TrEMBLrel. 10, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope 01ycoprotein immunodominant region (Fragment).
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14811 MW; F154B211B9D456D5 CRC64;
                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBL_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Best Local Similarity 96.2*
Matches 25; Conservative
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Matches 25; Conservative
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122 AA;
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C STRAIN=UG;

Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,

Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;

"Similar distribution and continued predominance of HIV-1 subtypes A rad D infections in Uganda.";

"Similar distribution and continued predominance of HIV-1 subtypes A rad D infections in Uganda.";

"Similar distribution and continued predominance of HIV-1 subtypes A rad D infections in Uganda.";

"Submitted (SEP-2000) to the MEDI/GenBank/DDBJ databases.

"BABL; AF307674; AAL08735.1;

"S OG (GO16021; C:integral to membrane; IEA.

"R OG (GO:0019031; C:viral envelope; IEA.

"R OG (GO:0019031; C:viral envelope; IEA.

"R OG (GO:0005198; F:structural molecule activity; IEA.

"R DEMI: PRO0517; GP41; 1.
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                                                                                                                                                                     Pieniazek D., Yang C., Lal R.L.;
"Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O sholdes are alternate region for subtype determination.";
Isolates provides an alternate region for subtype determination.";
BMBL; API1358; AAD42753.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR00328; Env GP41; 1.
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99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 AA; 14807 MW; 7744F5AF97830718 CRC64;
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122 AA; 14740 MW; 33822EBC1A1A3ACE CRC64;
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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                                                                                                                   SEQUENCE FROM N.A.
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RESULT 132 Q91LK4 ID Q91LK4 Q91LK4

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Masciotra S., Livellara B., Belloso, W., Clara L., Tanuri A., Ramos A., Baggs J., Lial R., Pieniazek D.;
Baggs J., Lal R., Pieniazek D.;
Berosexual population in Buenos Aries, Argentina.";
AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
BMBL; AR72067; AR7426.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:000518; Fistructural molecule activity; IEA.
InterPro; IPR000328; Env GP41: 1.
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STRAIN-RAJOSEMPO125,
Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
                                                                                                                                                                                    Length 122;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein immunodominant region (Fragment).
                                                                1
122 122
122 AA, 14721 MW, 9F9F0AA594BDB4B6 CRC64;
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122 AA; 14733 MW; 89C6303ACD037238 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
                                                                                                                                                                              Score 138; DB 15;
Pred. No. 1.9e-13;
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Pred. No. 1.9e-13;
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96.2%; Pred. No. ...
... 1; Mismatches
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96.2%; Pred. No. 1...
1; Mismatches
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MEDLINE=20346416; PubMed=10890362;
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Best Local Similarity 96.2%,
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Matches 25; Conservative
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   Pfam; PF00517; GP41; 1
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Q91JQ8
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C STRAIN=GP41ERRJ04;
C Caride E., Hertog6 E., Hartog6 E., Hartog6 E., Hertog6 E., H
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122 AA; 14834 MW; 13711994A52A5B33 CRC64;
                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses, Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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     99.3%; Score 138; DB 15;
1 Similarity 96.2%; Pred. No. 1.9e-13;
25; Conservative 1; Mismatches 0;
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1 RILAVERYLKDQQLLGIWGCSGKLIC
                                   PRT;
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Tanuti A., Swanson P.A., Devare S.G., Berro O.J., Savedra A., Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D., Rayfield M.;

"HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, ARC79298-11, -.
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0015198; F:structural molecule activity; IEA.
InterPro; IPR00328; Env_GP41.
         Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                             SEQUENCE FROM N.A. STRAIN=RJ96BRP030;
                        NCBI_TaxID=11676;
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GO: GO:0016021, Cintegral to membrane; IEA.

GO: GO:0016021, Cintegral to membrane; IEA.

GO: GO:001991; C:viral envelope; IEA.

InterPro; IPR000328; Env. GP41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
         "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."; blubitypes among blood donors from Rio de Janeiro, Brazil."; blubityted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0019031; C:viral envelope; IEA.

GO, GO:005199; F:structural molecule activity; IEA.

Interpro; IRR000228; Env_GP41.

Pfam; PF00517; GP41; 1.
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99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels
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122 AA; 14795 MW; 313ED9A97EB3167C CRC64;
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122 122
122 AA; 14712 MW; 960D670EAFASIF06 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein immunodominant region (Fragment).
                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
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NCBL TaxID=11676;
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Human immunodeficiency virus 1.
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Q90DN0
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Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
Cocta L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
Rayfield M.;
"HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
"HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
BMBL; AR034054; AAC73906.1; --
GO; GO:0010031; C:integral to membrane; IEA.
GO; GO:0010931; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Bnv_GP41; 1.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein immunodominant region (Fragment).
                                         122 AA; 14635 MW; 906927994C59310A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 122
122 AA; 14678 MW; A7C3D4FC2CE00A3D CRC64;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Best Local Similarity 96.29
Matches 25; Conservative
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SEQUENCE FROM N.A.
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ID Q90DI9
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122 122
122 AA; 14778 MW; DCBAE743D5815680 CRC64;
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EMBL, AR307742; AALO8031; C.
GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0019031; C:viral envelope; IEA.

GO, GO:005198; F:structural molecule activity; IEA.

InterPro; IPR000328; Env_GP41: 1.
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99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels
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122 Aa; 14684 MW; 71EA72685F2915C3 CRC64;
               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                          Viruses, Retroid viruses, Retroviridae, Lentivirus
NCBI_TaxID=11676,
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                                                                        Envelope glycoprotein (Fragment).
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                                                                                                           Human immunodeficiency virus 1.
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Q90DN2
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Masciotra S., Livellara B., Belloso, W., Clara L., Tanuri A., Ramos A., Baggs J., Lal R., Pieniazek D.;
Baggs J., Lal R., Pieniazek D.;
"Evidence for a high frequency of Englese P. infections among heterosexual population in Buenos Aries, Argentina.";
AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
BMBL, AF220675; ARFAZZ7.1; -
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0019031; C:viral envelope; IEA.
GO, GO:0051938; F:structural molecule activity; IEA.
FIREPEC: IPR000328; Env_GP41: 1.
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"HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF034039; AAC79291.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR00328; F:structural molecule activity; IEA.
Pfam; PP00517; GP41; 1.
                                                                                                                                                                                                                                                                                                                 [1] — SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=RJ96ERP009; Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A., Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
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                                                       01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MIN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein immunodominant region (Fragment).
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122 AA; 14739 MW; 40D4789EBBC88BC2 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein gp41 (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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PRELIMINARY;
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Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dorn J., Fridlund C., Shrahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.; "Similar distribution and continued predominance of HIV-1 subtypes A submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF307663; AAL08724.1; -
GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0019031; C:viral envelope; IEA.

GO: GO:001988; F:structural molecule activity; IEA.

Pfam; PF00517; GP41; 1.
                                                                                                                                            99.3%; Score 138; DB 15; Length 122; 96.2%; Pred. No. 1.9e-13; Live 1; Mismatches 0; Indels (
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                                                                                                             122 AA; 14693 MW; D20268AD4ADF8DEE CRC64;
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122 AA; 14719 MW; 2DDC88CBD61B23B0 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein immunodominant region (Fragment).
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VGD _TaxID=11676;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCRI_TaxID=11676;
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Best Local Similarity 96.2%
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EMBL, AF307664; AAL08725.1; --
GO; GO:0016021; C:integral to membrane; IEA.
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         Score 138; DB 15; Length 122; Pred. No. 1.9e-13; 1; Mismatches 0; Indels (
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Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches
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122 AA; 14755 MW; 0D30DB46BF54A8FA CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VSB_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBL_TaxID=11676;
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      ch 99.3%;
L Similarity 96.2%;
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RESULT 146 Q90DR7

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SEQUENCE FROM N.A.
C STRAIN=GP41ERR118;
Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
A machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
A calazans A.R., Tanuri A.;
Genotyping and phenotyping analysis of B and non-B Human
Immunodeficiency virus type I subtypes from patients under HAART.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
I Submitted (JUL-1999) to compare the EMBL, ART6851; ART6851; PR GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0015031; C:integral to membrane; IEA.
R GO; GO:005199; P:structural molecule activity; IEA.
R InterPro; IPR000328; ENV GP41.
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                         Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                            "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF034052; AAC79304.1; --
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0015031; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000328; Env_GP41:
PFam; PF00517; GP41; 1.
Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
Rayfield M.,
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
FIREPRO! GO:00517; GP41; 1.
                                                                                                                                                                                                                                                                                                                    122 AA; 14792 MW; 7D5BB60146B8FD17 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Best Local Similarity 96.2<sup>3</sup>
Matches 25; Conservative
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EC STRAIN=AR43;

X MEDLINE=20346416; PubMed=10890362;

X MBEDLINE=20346416; PubMed=10890362;

X MBEDLINE=20346416; PubMed=10890362;

X MASCIOTRA S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,

X Baggs J., Lal R., Pieniazek D.;

RT "Evidence for a high frequency of HIV-1 subtype F infections among RT "Evidence for a high frequency of HIV-1 subtype F infections among RT heterosexual population in Buenos Aries, Argentina.";

RIA AIDS Res. Hum. Retroviruses 16:1007-1014(2000).

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0016021; C:viral envelope; IEA.

DR GO; GO:0015031; C:viral envelope; IEA.

DR GO; GO:0015031; C:viral molecule activity; IEA.

DR HEAD; PF00517; GP41; 1.
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                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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122 AA
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RESULT 152 Q9EA95

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STRAIN-UG;
Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
"Similar distribution and continued predominance of HIV-1 subtypes A
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EMBL, AF307740; AALO8801.1; -

GO, GO:0015021; C:integral to membrane; IEA.

GO, GO:0015031; C:integral to membrane; IEA.

GO, GO:0015031; C:integral molecule activity; IEA.

InterPro; IPR000328; ENV_GP41.
     Length 122;
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                                           0; Indels
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF307673; AAL08731.;
GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:integral to membrane; IEA.
Interpro; IFR00328; Enructural molecule activity; IEA.
Pfam; PF00517; GP41; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Viruses; Retroid viruses; Retroviridae; Lentivirus
 99.3%; Score 138; DB 15;
96.2%; Pred. No. 1.9e-13;
iive 1; Mismatches 0;
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Best Local Similarity 96.24
Matches 25; Conservative
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WEDLINE=20134570; PubMed=10669328;

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WEDLINE=20134570; PubMed=10669328;

WEDLINE=20134570; PubMed=10669328;

A Waidle Pu', Games C.E., Irwin K.L., Pieniazek D., McGowan J.P.,

A Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;

The sence of human immunodeficiency virus (HIV) type 1, group M, non-B and types. Bronx, New York: a sentinel site for monitoring HIV genetic diversity in the United States.";

J. Infect. Dis. 181:470-475 (2000).

REMBL; AF190957; AAG02139:1;

G GO: GO:0019031; C:viral envelope; IEA.

GO: GO:0019031; C:viral envelope; IEA.

SR GO: GO:001598; F:structural molecule activity; IEA.

InterPro; IPR000328; Env_GP41.

P. Fam: PP00517; GP41; 1.
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99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels
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122 AA; 14767 MW; 363549B0844EDEE5 CRC64;
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122 122
122 AA; 14712 MW; 34B609D400C67CC5 CRC64;
                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                             Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
                                     122 AA.
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Pfam; PF00517; GP41; 1:
                                 PRELIMINARY;
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Best Local Similarity 96.23,
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Q91JN7
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AC 090DS6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tanuria. A., Swanson P.A., Devare S.G., Berro O.J., Savedra A., Tanuria. A., Swanson P.A., Devare S.G., Berro O.J., Savedra A., Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D., Rayfield M.;

Rayfield M.;

"HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

GO, GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; E:structural molecule activity; IEA.

InterPro: IPR000328; Env_GF41: 1.
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                                                                                                                               99.3%; Score 138; DB 15; Length 122; 96.2%; Pred. No. 1.9e-13; ive 1; Mismatches 0; Indels (
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein immunodominant region (Fragment).
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122 AA; 14571 MW; ASE7A49C0F1BA3AF CRC64;
                                                               122 122.
122 AA; 14816 MW; 6BD0DF2301B4043A CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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                                                                                                                                                 Local Similarity 96.2
les 25; Conservative
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Pfam; PF00517; GP41; 1.
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Matches
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Brond, C. olinegral to membrane, IEA.
GO, GO:0015031; C:viral envelope; IEA.
GO, GO:0015031; C:viral envelope; IEA.
Entructural molecule activity; IEA.
Franction Proposity, GP41; 1.
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122 12
122 AA; 14664 MW; 637EF68FDDC36A11 CRC64;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
Transmembrane.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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NCBI_TaxID=11676,
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                           99.3%; Score 138; DB 15; 3 96.2%; Pred. No. 1.9e-13; tive 1; Mismatches 0;
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Pred. No. 1.9e-13;
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96.2%; Pred. No. ...
1; Mismatches
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Hu D.G., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C., Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.; "Similar distribution and continued predominance of HIV-1 subtypes A submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, ARSOTAT3, AALO8792.1; -
EMBL, ARSOTAT3, AALO8792.1; -
EMBL, Colour C.integral to membrane, IEA.

GO, GO:0016021 C:integral to membrane, IEA.

GO, GO:0015081 F:structural molecule activity; IEA.

InterPro: IFR000328; ENV GP41.

Fransmembrane.
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EMBL, AP307668, AAL0829.1; -
GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0051981; Estructural molecule activity; IEA.

Probert, IPR000328; ENV.GP41: 1.
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 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                  Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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96.2%; Pred. No. 1.9e-13;
tive 1; Mismatches 0;
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                                   Envelope glycoprotein (Fragment).
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                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=UG;
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SEQUENCE
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Q90DR3;
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                                 Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dorn J., Fridlund C., Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.; "Similar distribution and continued predominance of HIV-1 subtypes A and D infections in Uganda."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF307655, AAL08716.1; --
GO; GO:0010611; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
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EMBL; AF307688; ABL0849.1; ---
GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:005198; F:structural molecule activity; IEA.

PF00517; GP41; 1.
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122
14818 MW; ACSDIEGC79749B83 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
ViCBL_TaxID=11676;
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Matches 25; Conservative
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STRAIN=ZIM29;
MEDLINE=20284721; PubMed=10826488;
Downing R., Pleniazek D., Hu D.J., Biryahwaho B., Fridlund C.,
Rayfield M.A., Sempala S.D., Lal R.B.;
"Genetic characterization and phylogenetic analysis of HIV-1 subtype C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C., Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.; "Similar distribution and continued predominance of HIV-1 subtypes A and D infections in Uganda.";
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122 AA; 14703 MW; 26D08CB693C40653 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCB_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
Score 138; DB 15;
Pred. No. 1.9e-13;
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AIDS Res. Hum. Retroviruses 16:815-819(2000).
ERBL; #57206062; AAR82018.1; Government Co. Government Co. Integral to membrane; IEA.
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Query Match
99.3%; Score 138; DB
Best Local Similarity 96.2%; Pred. No. 1.9e
Matches 25; Conservative 1; Mismatches
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Matches 25, Conservative
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Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
Birilar distribution and continued predominance of HIV-1 subtypes A and D infections in Uganda.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307669; ALL08730.1;
GO: GO: 0016021; C: integral to membrane; IEA.
GO: GO: 0019031; C: viral envelope; IEA.
GO: GO: 0005198; F: structural molecule activity; IEA.
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122 AA; 14718 MW; E822C25F0AAE61F1 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Pfam; PF00517; GP41; 1.
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Matches 25, Conservative
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Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
"Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
diversity in the United States.";
J. Infect. Dis. 18:470-475(2000).
EMBL; AF190964; AAG02326.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env. GP41.
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                 MEDLINE=20134570; PubMed=10669328;
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MEDLINE=20346416; PubMed=10890362;
MasDiotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
Baggs J., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
Baggs J., Lal R., Pieniazek D.;
"Evidence for a high frequency of HIV-1 subtype F infections among
heterosexual population in Buenos Aries, Argentina.";
AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
EMBL, AF220686, AAF74238.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016031; C:integral to membrane; IEA.
GO; GO:0016031; C:integral molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
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122 12
122 AA, 14746 MW, 194509B404DDC61B CRC64;
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14729 MW; DICF7E2498427841 CRC64;
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPRO0228; Env_GP41.
Pfam; PF00517; GP41; 1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein gp41 (Fragment).
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope 91ycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Q9EA88;
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EMBL, AF307660; AAL08721.1; GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0019031; C:viral molecule activity; IEA.

Pfam; PF00517; GP41; 1.
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122 Aa; 14727 MW; 63657CA763C369EF CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNI-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                                                                          122 AA
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19 RVLAVERYLKDQQLLGIWGCSGKLIC 44
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                                                                                                                          PRT;
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Best Local Similarity 96.2:
Matches 25; Conservative
                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Q91JQ6
ID Q91JQ6
AC Q91JQ6
DT 01-OCT
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19 RVLAVERYLKDQQLLGIWGCSGKLIC 44
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SEQUENCE FROM N.A.
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Q90DK2
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STRATIS_ARAB9;

MEDLINE=20346416; PubMed=10890362;

A Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A., Baggs J., Lal R., Pieniazek D.;

"Evidence for a high frequency of HIV-1 subtype F infections among T. heterosexual population in Buenos Aries, Argentina.";

AIDS Res. Hum. Retroviruses 16:1007-1014(2000).

REMBL, AF220677; AAF742291; -.

REMBL, AF220677; AAF742291; -.

REMBL, AF220677; C:integral to membrane; IEA.

GO; GO:0015081; C:integral to membrane; IEA.

RO; GO:001598; Estructural molecule activity; IEA.

REMBL: PF00517; GP41; 1.
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                                                                                                                             MEDLINE=20346416; PubMed=10890362;
Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
Baggs J., Lal R., Pieniazek D.;
"Evidence for a high frequency of HIV-1 subtype F infections among
heterosexual population in Buenos Aries, Argentina.";
AIDS Res Hum. Retroviruses 16:1007-1014(2000).
EMBL; AF220676; AAF74228.1;
GO; GO:0018031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005189; F:structural molecule activity; IEA.
InterPro; IPR000238; Env_GP41.
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99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels
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122 AA; 14841 MW; 6752EF2965DD4709 CRC64;
                                                                                                                                                                                                                                                                                                                                      122 AA; 14844 MW; DCB555869433C0EF CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Envelope glycoprotein gp41 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein gp41 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
                                                  Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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                                                                                                       SEQUENCE FROM N.A.
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091JQ5;
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Q91JQ5
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1 RILAVERYLKDQQLLGIWGCSGKLIC 26

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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF307700; AAL08761.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IFR00328; Env. GP41.
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122 122
122 AA; 14668 MW; 9AB027886DFBEA73 CRC64;
                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                            Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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122 AA
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hes 25; Conservative
PRELIMINARY;
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Q91JP2
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Q90DS7
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GO; GO:0016021; C:integral to membrane; IEA.
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122 AA; 14684 MW; AEBB7D3AE1B0BE23 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-JUN-2003
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MEDLINE=20346416; PubMed=10890362;

Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
Baggs J., Lal R., Pienniazek D.;

"Evidence for a high frequency of HIV-1 subtype F infections among
heterosexual population in Buenos Aries, Argentina.";
AIDS Res. Hum. Retroviruses 16:1007-1014(2000).

EMBL; AF220690; AAF76809-1;
GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:00519031; E:mr. Grant molecule activity; IEA.

FIREPRO: IPR000328; Env. GP41.
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122 AA; 14848 MW; FEF3F75550D01A63 CRC64;
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122 AA; 14748 MW; 61E64BBC3F42460A CRC64;
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:sEructural molecule activity; IEA.
InterPro; IPRO0328; Env_GP41.
Pfam; PF00517; GP41; 1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Bnvelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Matches 25; Conservative
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Matches 25; Conservative
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Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos Jagos J., Lal R., Pieniazek D.;
Baggs J., Lal R., Pieniazek D.;
Fredence for a high frequency of HIV-1 subtype F infections among heterosexual population in Buenos Aries, Argantina.";
AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
BMBL, AF206681, AAF74233.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000128; Extuctural molecule activity; IEA.
PF00517; GP41; 1.
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122 AA; 14676 MW; D2B27F903F4EB2AD CRC64;
 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein gp41 (Fragment).
                      Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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A Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
A Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
Calazans A.R., Tanuri A.;
T. "Genotyping and phenotyping analysis of B and non-B Human
I immunodeficiency virus type 1 subtypes from patients under HART.";
L Submitted (JULI-1999) to the BMBL/GenBank/DDBJ databases.
E EMBL; AR165557; AAF08502.1;
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0019031; C:viral envelope; IEA.
R GO; GO:005199; F:structural molecule activity; IEA.
R InterPro; IPR000228; Env_GP41.
          Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C., Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.; "Similar distribution and continued predominance of HIV-1 subtypes A submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0015031; C:integral to membrane; IEA.

FEMPL, PRO0517; GF41; 1.
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122 AA; 14861 MW; CE141BE5AF77D68C CRC64;
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122 AA; 14635 MW; D052E4B73AE3008E CRC64;
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01-MAY-2000 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-JUN-2003 (TYEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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NCBI_TaxID=11676;
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Score 138; DB 15; Pred. No. 1.9e-13; 1; Mismatches 0;

Length 122;

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"Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O isolates provides an alternate region for subtype determination.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR113581; AAD42749.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0015031; C:viral envelope; IEA.
InterPro; IPR000328; Erstructural molecule activity; IEA.
Pfam; PP00517; GP41; 1.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                     Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Pred. No. 1.9e-13;
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96.2%; Pred. No. 1...
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Query Match
Best Local Similarity 96.2°
Matches 25; Conservative
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Q91JQ9
ID Q91JQ9
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Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
Bagge J., Lal R., Pientazek D.;
Evidence for a high frequency of HIV-1 subtype F infections among
heterosexual population in Buenos Aries, Argentina.";
ATDS Res. Hum. Retroviruses 16:1007-1014(2000).
EMBL; AF220721; AAF76840.1;
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:00588; F:structural molecule activity; IEA.
FRAME 
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Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
Baggs J., Lal R., Pientazek D.;
"Evidence for a high frequency of HIV-1 subtype F infections among
heterosexual population in Buenos Aries, Argentina.";
AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
EMBL; AF220703; AAF76822.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:000518; F:structural molecule activity; IEA.
InterPro; IPR00028; Env. GF41: 1.
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99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels (
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14679 MW; ABE4BB421A98FFA5 CRC64;
                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                       01-OCT-2000 (TrEMBLrel. 15, Crea Ol-OCT-2000 (TrEMBLrel. 15, Last Ol-UUN-2003 (TrEMBLrel. 24, Last Envelope glycoprotein (Fragment)
                                    PRELIMINARY;
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                                                                     01-0CT-2000
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Baggs J., Lal R., Pieniazek D.;
Baggs J., Lal R., Pieniazek D.;
Brescherosexual population in Buenos Aries, Argentina.";
AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
BMBL, AP220673; AAF74255.1;
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0019031; C:viral envelope; IEA.
GO, GO:0019031; C:viral envelope; IEA.
FILEAPERO; IPR000328; F:structural molecule activity; IEA.
PF00517; GP41: 1.
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MEDLINE=20346416; PubMed=10890362;
Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
Evidence for a high frequency of HIV-1 subtype F infections among
heterosexual population in Buenos Aries, Argentina.";
AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
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      Length 122;
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                                                             Indels
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein gp41 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
99.3%; Score 138; DB 15; 36.2%; Pred. No. 1.9e-13; ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                122 AA
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MEDLINE=20346416; PubMed=10890362;
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Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C., Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.; "similar distribution and continued predominance of HIV-1 subtypes A and D infections in Uganda. BEL/GenBank/DDBJ databases.

EMBL, AR307649, AALGORST10.1; C. integral to membrane; IEA.

GO: GO:0016021; C:integral to membrane; IEA.

GO: GO:0019031; C:viral envelope; IEA.

GO: GO:0015038; F:structural molecule activity; IEA.

Interpro; IPRO0328; Env. GP41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
"HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
BMBL; AF034060; AAC79312.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR00328; Env_GP41.
Pfam; PF00517; GP41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
Rayfield M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 122;
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122 AA; 14713 MW; A6117281CEA10231 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1993 (TrEMBLrel. 4, Last annotation update)
Envelope glycoprotein immunodominant region (Fragment)
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122 AA; 14701 MW; 4EED351A06F7C74F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.3%; Score 138; DB 15;
96.2%; Pred. No. 1.9e-13;
iive 1; Mismatches 0;
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96.2%; Pred. No. 1.9e-13;
iive 1; Mismatches 0;
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Q9EA82;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
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Best Local Similarity 96.2%
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     SEQUENCE FROM N.A.
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                                     STRAIN=UG;
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Q9EA82
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                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                              Match 99.3%; Score 138; DB 15; Length 122; Local Similarity 96.2%; Pred. No. 1.9e-13; les 25; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                             122 AA; 14749 MW; 810E603A372AA8C4 CRC64;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:001998; Faructural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
PF00517; GP41; 1.
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AIDS Res. Hum. Retroviruses 16:815-819(2000).
EMBL, APZ061001.
GO; GO:01016021, C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005189; F:structural molecule activity; IEA.
PITTEPPO. TERFO00328; Env. GP41.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                                                                                            Transmembrane.
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STRAINEARS3;

MEDLINE=20346416; PubMed=10890362;

MEDLINE=20346416; PubMed=10890362;

Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,

Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,

Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,

Exidence for a high frequency of HIV-1 subtype F infections among I berioscaral population in Buenos Aries, Argentina.";

Intercoscaral population in Buenos Aries, Argentina.";

EMBL, AF220678; AAF74230.1;

CG, GO:001601; C:integral to membrane; IBA.

GO; GO:0019031; C:viral envelope; IBA.

RO; GO:005198; F:structural molecule activity; IEA.

InterPro; IPR000328; Env_GP41.

Transmembrane.
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BMBL, AR907708, AAL08769.1, -
GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0019031; C:viral envelope; IEA.

GO, GO:0019031; C:viral molecule activity; IEA.

FIREPRO, IPR000328; Env_GP41.
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122 AA; 14703 MW; 834721661D3A360E CRC64;
                                                                                                                                                                                                                                                                                                Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein gp41 (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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         19 RVLAVERYLKDQQLLGIWGCSGKLIC 44
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Best Local Similarity 96.2*,
-hes 25; Conservative
                                                                                                                          PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                     Q91JQ4;
Q91JQ4;
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                                                                              RESULT 190
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X MEDLIRE_20134570; PubMed=10669328;

Medlo P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,

A Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;

Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;

"Presence of human immunodeficiency virus (HIV) type 1, group M, non-B rubtypes, Bronx, New York: a sentinel site for monitoring HIV genetic diversity in the United States."

I J. Infect. Dis. 181:470-475 (2000).

EMBL, AF190970; AAG02332.1; -

ROG GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

ROG GO:0019031; C:viral envelope; IEA.

ROG GO:0019031; C:viral envelope; IEA.

ROG GO:0005198; Fistuctural molecule activity; IEA.

Pefam; PF00517; GP41; 1.
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Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
Hu D.J., Baggs J., Downing R.G., Rayfield M.A., Dondero T.J., Lal R.;
Biryahwaho B. S., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
"Similar distribution and continued predominance of HIV-1 subtypes A and D infections in Uganda.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR307724; AALGR785.1; ---
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:viral envelope; IEA.
GO; GO:001931; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
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99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0
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99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred. No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 AA; 14804 MW; CF6AF2DC9EDA9C69 CRC64;
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122 AA; 14750 MW; 10D65E3EF7D41A9E CRC64;
01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Envelope glycoprotein (Fragment).
                                                                                  Viruses, Retroid viruses; Retroviridae, Lentivirus.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                Human immunodeficiency virus 1.
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P. SEQUENCE FROM N.A.
STRAIN-RAJ97BRP105;
A Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
A Rayfield M.;
"HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
I. Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
I. Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
R. GO; GO:0019031; C:integral to membrane; IEA.
R. GO; GO:0019031; C:viral envelope; IEA.
R. GO; GO:0005198; Fstructural molecule activity; IEA.
R. InterPro; IPR000328; Env_GP41.
R. Pfam; PF00517; GP41; 1.
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STRAIN=GP41ERRJ23;
Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
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122 AA; 14857 MW; 1FC64594F75A207C CRC64;
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GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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NCB__TaxID=11676;
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Pred. No. 1.9e-13;
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Matches 25, Conservative
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Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
Baryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
Birmilar distribution and continued predominance of HIV-1 subtypes A and D infections in Uganda.";
Submitteed (SSP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR307715; AAL0876.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IRR000228; Bnv_GP41: 1.
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"Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O isolates provides an alternate region for subtype determination.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF113588; AAD42756.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
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           122 AA; 14603 MW; 3DDFA4A8CEC96CB7 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                               99.3%; Score 138; DB 15; 96.2%; Pred. No. 1.9e-13;
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                                                                                               Best Local Similarity
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RESULT 193 Q9WQZ4

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Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C., Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R., "Similar distribution and continued predominance of HIV-1 subtypes A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.3%; Score 138; DB 15; Length 122; 96.2%; Pred. No. 1.9e-13;
                                                                                                                                                                                                                                        and Dinfections in Uganda.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF307696, AAL08075.1;
GO, GO:0016021; C:integral to membrane, IEA.
GO, GO:0019031; C:viral envelope; IEA.
GO; GO:001998; F:structural molecule activity; IEA.
InterPro; IFR00328; Env GP41.
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                                        Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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NCBI_TaxID=11676;
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EMBL, AF307693; AAL08754.1; -
GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0051989; Fstructural molecule activity; IEA.

Pfam; PF00517; GP41; 1.
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Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A., Calazans A.R., Tanuri A.;
"Genotyping and phenotyping naulysis of B and non-B Human immunodeficiency virus type I subtypes from patients under HAART."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, AR165556; AR268501.1; --
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
Pfam; PR00517; GP41; 1.
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122 AA; 14719 MW; BIA827E231D3748D CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Baggs J., Lal R., Pieniazek D.;
"Evidence for a high frequency of HIV-1 subtype F infections among heterosexual population in Buenos Aries, Argentina.";
AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
BMBL; AP220685; AAF74237.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:000318; F:structural molecule activity; IEA.
FIREPERS: IPR000328; Env GP41.
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122 122
122 AA; 14704 MW; 5538AD9D2B012589 CRC64;
                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein gp41 (Fragment).
                                                                                                                                                                                                            Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
   122 AA.
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1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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STRAIN=UG95-327;
STRAIN=UG95-327;
SWARSON P.A., Devare S.G., Hackett J.R. Jr.;
Wholecular Characterization of 39 HIV-1 Isolates Representing Group M [Subtypes A.G) and Group O. Sequence Analysis of gag p24, pol integrase, and env gp41.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY214083; AAO61803.1; -.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198 F:structural molecule activity; IEA.
InterPro; IPR000328; ENV_GP41.
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STRAIN=UG;
Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C., Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.; Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.; Similar distribution and continued predominance of HIV-1 subtypes A and Diffections in Uganda."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AR30719; AAL06780.1; --
GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016198; F:structural molecule activity; IEA.

InterPro; IPR006128; Env_GP41.
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99.3%; Score 138; DB 15; Length 122;
Best Local Similarity 96.2%; Pred..No. 1.9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels
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122 AA; 14748 MW; 68F4BCCA8DC1DBC0 CRC64;
                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                       Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Best Local Similarity 96.2%,
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Swanson P.A., Devare S.G., Hackett J.R. Jr.;
"Molecular Characterization of 39 HIV-1 Isolates Representing Group M
"Molecular Characterization of 39 HIV-1 Isolates Representing Group M
(Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol
integrase, and env gp41.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY214087; AA061807.1;
GO; GO:0019011; C:viral envelope; IEA.
InterPro; IRR000328; Env GP41.

Pfam; PF00517; GP41; 1.
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Swanson P.A., Devare S.G., Hackett J.R. Jr.;
"Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, polintegrase, and env gp41.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AN214088, AAG61808.1;
GO; GO:0019931; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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122 122
122 AA; 14675 MW; 4E83B592C7C10ACB CRC64;
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NOB_TaxID=11676;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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NCBI_TaxID=11676;
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19 RVLAVERYLKDQQLLGIWGCSGKLIC 44
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Pfam; PF00517; GP41; 1.
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Swanson P.A., Devare S.G., Hackett J.R. Jr.;
"Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, polintegrase, and env gp41.";
Submitted (JAN-22003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY214092; AA061812.1;
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0051981; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
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122 AA; 14786 MW; 6C4FAFF8579F9104 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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96.2%; Pred. No. 1.9e-13;
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Pfam; PF00517; GP41;
Envelope protein.
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SWANDON P.A., Devare S.G., Hackett J.R. Jr.;
SWANDON P.A., Devare S.G., Hackett J.R. Jr.;
Wolecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O. Sequence Analysis of gag p24, pol integrase, and env gp41.";
Submitted (JAW-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY214089; AA618091; ...
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41: 1.
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SWAINSON P.A., Devare S.G., Hackett J.R. Jr.;
Wolecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group.0. Sequence Analysis of gag p24, pol integrase, and env gp41.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY214091; AAO61811.1;
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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122 AA; 14674 MW; 95E8C3532B34165F CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Swanson P.A., Devare S.G., Hackett J.R. Jr.;
Swanson P.A., Devare S.G., Hackett J.R. Jr.;
"Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, polintegrase, and env gp41.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY214119; AA061839.1; ---
GO; GO:001931; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.

Pfam; PF00517; GP41; 1.
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"Molecular epidemiology of HIV-1 infection in Portugal: high prevalence of non-B subtypes.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ318198; CAC685977.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:001989; F:structural molecule activity; IEA.
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123 AA; 14914 MW; C94786EC61260642 CRC64;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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Pred. No. 1.9e-13;
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"Molecular Characterization of 39 HIV-1 Isolates Representing (Subtypes A-G) and Group O: Sequence Analysis of gag p24, polintegrase, and env gp41.";

Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY214094; AA061814.1;

GO; GO:0019131, C:vixal envelope; IEA.

GO: GO:005198; F:structural molecule activity; IEA.

InterPro; IPR000328; Env GP41.

Pfam; PF00517; GP41; 1.
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1 Similarity 96.2%; Pred. No. 1.9e-13;
25; Conservative 1; Mismatches 0; Indels
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integrase, and env gp41."; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AY214093; AAO61813.1; -. GO; GO:0019031; C:viral envelope; IEA. GO; GO:0005198; F:structural molecule activity; IEA. InterPro; IRR000328; Env_GP41.
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122 AA; 14767 MW; 038D675003BEC8A5 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
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Envelope glycoprotein (Fragment).
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Esteves A., Parreira R., Venenno T., Franco M., Piedade J.,
Germano de Sousa J., Canas-Ferreira W.,
"Genetic diversity of HIV-1 spreding among intravenous drug users in
Lisbon, Portugal.";
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A de Sousa G., Canas-Perreira W., Venenno T., Franco M., Piedade J.,

Bateves A., Parreira R., Venenno T., Franco M., Piedade J.,

A de Sousa G., Canas-Perreira W.;

"Molecular epidemiology of HIV-1 infection in Portugal: high
prevalence of non-B subtypes.";

I Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ118399; CAC65978.1;

R GO; GO:0019031; C:irial envelope; IEA.

R GO; GO:0019031; C:irial envelope; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

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123 AA; 14862 MW; 0F1E4342A90F42C9 CRC64;
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                                     01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                    Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                              Gp41 (Fragment).
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
GO: 00016021; C:integral to membrane; IEA.
GO: GO:0019031; C:viral envelope; IEA.
GO: 0005198; F:structural molecule activity; IEA.
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Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
Rayfield M.;
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                                                                                           ESCUENCE FROM N.A.

ESTEVES A., Parreira R., Venenno T., Franco M., Piedade J., de Sousa G., Canas-Ferreira W.;

"Molecular epidemiology of HIV-1 infection in Portugal: high prevalence of non-B subtypes.";

Submitted (UUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ318406; CAC85985.1;

GO; GO:0018031; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0019938; F:structural molecule activity; IEA.
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123 AA; 14791 MW; D79184FA768COE60 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein immunodominant region (Fragment)
         Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses: Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pfam; PF00517; GP41; 1.
Transmembrane.
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Pfam; PF00517; GP41; 1.
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RESULT 212 Q8J3S2

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STRAIN=85CD244;

A MEDLINE=21134754; PubMed=11242522;

A MEDLINE=21134754; PubMed=11242522;

Yang C., Dash B., Hannen S.L., Frances H.S., Nzilambi N.,

Colebunders R.C., St Louis M., Ouinn T.C., Folks T.M., Lal R.B.;

T con Kinshasa, Democratic Republic of Congo.";

AIDS Democratic Republic of Congo.";

AIDS Hun. Retroviruses 17:361-365(2001).

REMBL, AF260477; AAF71944.1;

RO; GO:0019031; C:integral to membrane; IEA.

RO; GO:0019031; C:viral envelope; IEA.

RO; GO:0019031; C:viral envelope; IEA.

RICHERPO: INFR000328; Envelope; IEA.

RICHERPO: INFR000328; Envelope; IEA.

Pefam; PF00517; GP41: 1.
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Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
"Predominance of HIV type 1 subtype G among commercial sex workers
from Kinshasa, Democratic Republic of Congo.";
AIDS Res. Hum. Retroviruses 17:361-365(2001).
EMBL, AF266467; AAF71934.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:001998; F:structural molecule activity; IEA.
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125 AA; 14805 MW; 4EB9BF1C23F33469 CRC64;
                                                                                                                                                             (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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NCBI_TaxID=11676,
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99.3%; Score 138; DB 15
Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches
                                                                                                                                  125 AA
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1; Mismatches
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MEDLINE=21134754; PubMed=11242522;
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STRAIN=140.223;
Bennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
Phillips J.R., Kataaha P.K., Jackson J.B., Devare S.G.;
"Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
                                                                                                                                                                                                    BEGUENCE FROM N.A.

Beteves A., Parreira R., Venenno T., Franco M., Piedade J.,
A de Sousa G., Canas-Perreira W.;
"Molecular epidemiology of H1V-1 infection in Portugal: high
prevalence of non-B subtypes.";
"Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases."
EMBL; AJ318404; CAC65983.1;
CG; GO:0019031; C:viral envelope; IEA.
RG; GO:0019031; C:viral envelope; IEA.
RG; GO:0005198; F:structural molecule activity; IEA.
RICEPRO; IPR000328; ENV GP41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       124 AA; 14833 MW; 1373000B4D608F5A CRC64;
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14820 MW; 37C85D6A080B393B CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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01-NOV-1999 (TrEMBLrel. 12, C.
01-NOV-1999 (TrEMBLrel. 12, L.
01-JUN-2003 (TrEMBLrel. 24, L.
Gp41 (Fragment).
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STRAIN=264.643;
Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.,
"Serclogic and Phylogenetic Characterization of HIV-1 Subtypes in
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STRAIN-85CD085;
MEDLINE-21134754; PubMed=11242522;
Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases. BMBL, AF006923; A-AD013671; -. Government of AF006921; Cintegral to membrane; IEA. GO; GO:0019031; C:integral to membrane; IEA. GO; GO:0019031; C:viral envelope; IEA. GO; GO:0005198; F:structural molecule activity; IEA. InterPro; IRR00328; Env_GP41.
                                                                                                126 AA; 15246 MW; A73CDFAAECC6E129 CRC64;
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127 AA; 15335 MW; A3422CAD00B2CFB7 CRC64;
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01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
VCBI_TaxID=11676;
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InterPro; IPR000328; Env_GP41.
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Best Local Similarity 96.23
Matches 25; Conservative
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                    Pfam; PF00517; GP41; 1
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Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
Prededminance of HIV type I subtype G among commercial sex workers
from Kinshasa, Demooratic Republic of Congo.";
AIDS Res. Hum. Retroviruses 17.361-365(2001).

EMBL; AR560466, AAF71933.1, -

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:005198; F:structural molecule activity; IEA.

InterPro; IPR00328; Env_GP41.

PEam; PF00517; GP41; 1.
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STRAIN=122.335;
Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
"Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
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Pred. No. 2e-13;
1; Mismatches 0; Indels (
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EMBL, AF006846; AAD01290.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
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127 AA; 15272 MW; 076E4A6CBABE822E CRC64;
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127 AA: 15296 MW; 6F8361B317E554CA CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676;
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MEDLINE-20386754; PubMed=10933623; MEDLINE-20386754; PubMed=10933623; Yang C., Gao F., Fonjungo P.N., Zekeng L., van der Groen G., Pieniazek D., Schable C., Lal R.B.; Pieniazek D., Schable C., Lal R.B.; Phylogenetic analysis of protease and transmembrane regions of HIV type 1 group O."; AIDS Res. Hum. Retroviruses 16:1075-1081(2000). BMBL, AF22203; AAF714571; -. Go, Go:0016021; C:integral to membrane; IEA. Go; Go:0016021; C:viral envelope; IEA. Go; Go:001598; Estructural molecule activity; IEA. Hum.PPO0517; GP41; 1.
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Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
"Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AFGOG6918, AAD01342.1;
GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IFR000328; Env GP41.
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                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                      Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Matches 25; Conservative
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                                                                                             STRAIN=102.938;
Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
"Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
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Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S., Phillips J.F., Katadha P.K., Jackson J.B., Devare S.G.;
"Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
BMBL, AP006937; AAD01381.1;
GQ, GQ:0016021; C:integral to membrane; IEA.
GQ; GQ:00191031; C:viral envelope; IEA.
GQ; GQ:0005198; F:sgructural molecule activity; IEA.
InterPor. CGD3138; ENV. GP41.
                                                                                                                                                                                           Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AF0066839; AAD010231.; ...
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR00328; Env_GP41.
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127 AA; 15243 MW; 325EDBCD3C504556 CRC64;
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127 AA; 15215 MW; A3CIDEBOCB5DCE00 CRC64;
Human immunodeficiency virus 1.
Viruses, Retroid viruses, Retroviridae, Lentivirus.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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MEDLINE=21134754; PubMed=11242522; MEDLINE=21134754; PubMed=11242522; Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N., Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.; "Predominance of HIV type 1 subtype G among commercial sex workers
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STRAIN=326.662;
Bremnan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
"Serologic and Phylogenetic Characterization of HIV-1 Subtypes in Uganda.";
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130 AA; 15662 MW; 33C9EE30DA2A98C4 CRC64;
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Last sequence update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI TaxID=11676;
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                                                                                                                                                                                                                                      25; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 25; Conserv
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       Transmembrane.
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099YW6
AC 099YW6
DT 01-MAY.
DT 01-MAY.
DT 01-UMA.
DE GP41 (1
GN HNMA)
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MDCLNE=21134754;
MDCLNE=21134754;
MDCLNE=21134754;
Wang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
"Predominance of HIV type I subtype G among commercial sex workers
from Kinshasa, Democratic Republic of Congo.";
RMBL, ARZ60460; ARAF1927.1;
GO; GO:0019031; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:000328; Estructural molecule activity; IEA.
PFR00517; GP41; I.
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Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S., Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.; "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches
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                     1 RILAVERYLKDQQLLGIWGCSGKLIC 26
                                                            26 RVLAVERYLKDQQLLGIWGCSGKLIC 51
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Q91WR6
AD Q91WR6
DT Q1-OCT
DT O1-OCT
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Human immunodeficiency virus 1.
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99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                             132 AA; 15607 MW; 6A05003B8A9F2B14 CRC64;
from Kinshasa, Democratic Republic of Congo.";
AIDS Res. Hum. Retroviruses 17:361-365(2001).
EMBL. AF260476; AAF71943:1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198] F:serructural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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EMBL; AF405152; ALG6672.1; -

EMBL; AF405152; ALG6672.1; -

GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:005198; F:structural molecule activity; IEA.

Elem; PF60517; GP41; 1.
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NCBI TaxID=11676;
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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STRAIN=002M148F;
MEDLINE=21602569; PubMed=11739704;
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01-MAR-2002 (TrEMBLrel. 20,
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Q8UQW8;
01-MAR-2002 (
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Q8UQW8
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Trask S.A., Derdeyn C.A., Fideli U., Chen Y., Meleth S., Kasolo F...
Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
"Molecular epidemiology of human immunodeficiency virus type 1
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Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
"Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
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Submitted (JUN.1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF006850; AAD01294.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
Figure.; IFR00328; Env. GP41.
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133 AA; 15931 MW; 184000DE06060C81 CRC64;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
PF00517; GP41; 1.
Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Pred. No. 2.1e-13;
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les 25; Conservative
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hes 25; Conservative
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RESULT 232

090018

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"Molecular Deptidemiology of HIV type 1 subtypes in Equatorial Guinea.";
AIDS Res. Hum. Retroviruses 17:851-855 (2001).
EMBL; AF331078; AAK92289.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
Fransmembrane.
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"Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";

AIDS Res. Hum. Retroviruses 1.851-855(2001).

EMBL, AF331148; AAK92559.1.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:001508; F:structural molecule activity; IEA.

InterPro; IPR000328; Env GP41.
    Gaps
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MEDLINE=21322034; PubMed=11429126;
Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
Garcia-Saiz A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=99ES-MO1617;
MEDLINE=21322034; PubMed=11429126;
Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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  1; Mismatches
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                                                                        36 RVLAVERYLKDQQLLGIWGCSGKLIC 61
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(TrEMBLrel. 19, Last seq
(TrEMBLrel. 24, Last ann
                                       1 RILAVERYLKDQQLLGIWGCSGKLIC
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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  25; Conservative
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les 25; Conservative
                                                                                                                                                                            PRELIMINARY;
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NCBI_TaxID=11676;
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01-DEC-2001
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Matches
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AIDS Res. Hum. Retroviruses 17:851-855 (2001).
EMBL; AF331123; AAK92334.1; --
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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STRAIN-95ES-W01475;
MEDLINE=21322034; PubMed=11429126;
Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E., Garcia-Saiz A.,
Garcia-Saiz A.,
"Molecular epidemiology of HIV type I subtypes in Equatorial Guinea.";
AIDS Res. Hum. Retroviruses 17:851-855(2001).
BMBL, AF331084, AAK92255.1;
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0018031; C:viral envelope; IEA.
GO, GO:00538; Fistructural molecule activity; IEA.
InterPro; IPR000328; Env_GP41: 1.
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STRAIN=99BS-MO1557;
MEDLINE=21322034; PubMed=11429126;
Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu B.,
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15765 MW; 8534092BDE8ADB4F CRC64;
                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                 133 AA.
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                                                                                                                             Envelope glycoprotein (Fragment).
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Best Local Similarity 96.23
Matches 25; Conservative
                               PRELIMINARY;
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Best Local Similarity
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SEQUENCE
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090057

RESULT 233

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Envelope glycoprotein (Fragment).
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Local Similarity 96.2%;
les 25; Conservative
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QBUQZ3;
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Q90Q25;
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Q90Q25
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"Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
AIDS Res. Hum. Retroviruses 17:851-855(2001).
EMBL, AR311104; AAK92115.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001931; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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STRAIN=98ZW043M;
MEDLINE=21602569; PubMed=11739704;
Trask S.A., Derdeyn C.A., Fideli U., Chen Y., Meleth S., Kasolo F.,
Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
"Molecular epidemiology of human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=99ES-MO1517;
MEDLINE=21322034; PubMed=11429126;
Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
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                                                                                       / Match 99.3%; Score 138; DB 15; Length 133; Local Similarity 96.2%; Pred. No. 2.1e-13; Nes 25; Conservative 1; Mismatches 0; Indels
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                                     133 133 133 134 13A163CF35C3D6F2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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  Transmembrane.
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Garcia-Saiz A.;
"Molecular epidemiology of HIV type I subtypes in Equatorial Guinea.";
"Molecular epidemiology of HIV type I subtypes in Equatorial Guinea.";
AIDS RES. Hum. Retroviruses 17:851-855(2001).
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:integral to membrane; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
Interbro; IPR000328; Env_GP41.
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STRAIN=99ES-MO1541;
MEDLINE=21322034; PubMed=11429126;
Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,
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transmission in a heterosexual cohort of discordant couples in
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                                                                                                                                                                                                                                                                                              133 AA; 16057 MW; 6650DBE2480703B0 CRC64;
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                                            J. Virol. 76:397-405 (2002).

EMBL, AF405154; AL66674.1;

EMBL, AF405154; AL66674.1;

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:iral envelope; IEA.

GO; GO:005198; F:structural molecule activity; IEA.

Fransmembrane.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676;
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Pred. No. 2.1e-13;
1; Mismatches 0;
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133 AA

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PROUGENCE FROM N.A.

SECURATE PROBLEM PubMed=11429126;

WEDLINE=21322034; PubMed=11429126;

MEDLINE=21322034; PubMed=11429126;

A Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu E.,

A Garcia-Saiz A.; Pum. Retroviruses 17:851-855(2001).

A IDS Res. Hum. Retroviruses 17:851-855(2001).

ROJ GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

ROJ GO:0019031; C:viral envelope; IEA.

ROJ GO:0005199; Pstructural molecule activity; IEA.

ROJ GO:0019031; C:viral envelope; IEA.

ROJ GO:0019031; C:viral envelope; IEA.

ROJ GO:0019031; C:viral envelope; IEA.

ROJ GO:0005199; Pstructural molecule activity; IEA.
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MEDLINE-2132034; PubMed=11429126;
Ortiz M., Sanchez I., Gonzalez M.P., Leon M.I., Abeso N., Asumu B.,
Garcia-Saiz A.;
"Molecular epidemiology of HIV type 1 subtypes in Equatorial Guinea.";
AIDS Res. Hum. Retroviruses 17:851-855 (2001).
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001991; C:integral to membrane; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; ENV_GP41:
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133 AA; 15658 MW; 200E088E3482A65A CRC64;
                                                                                                                                  (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                          Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                               PRELIMINARY;
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es 25; Conservative
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133 AA;
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01-DEC-2001 (
01-JUN-2003 (
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Q90Q27;
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                       RESULT 241
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MEDLINE=21134754; PubMed=11242522;

MEDLINE=21134754; PubMed=11242522;

A Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,

Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;

T from Kinshasa, Democratic Republic of Congo.";

LAIDS Res. Hum. Retroviruses 17:361-365(2001).

R RGD: GO:0016021; C:integral to membrane; IEA.

R GO: GO:0016021; C:integral to membrane; IEA.

R GO: GO:0016913; C:integral to membrane; IEA.

R GO: GO:0016918; F:structural molecule activity; IEA.

R InterPro; IPR000328; Env GP41.
                                                                                                                                                                     Trask S.A., Derdeyn C.A., Fideli U., Chen Y., Meleth S., Kasolo F., Musonda R., Hunter E., Gao F., Allen S., Hahn B.H., "Molecular epidemiology of human immunodeficiency virus type 1 transmission in a heterosexual cohort of discordant couples in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Local Similarity 96.2%; Pred. No. 2.1e-13;
les 25; Conservative 1; Mismatches 0; Indels
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99.3%; Score 138; DB 15; Length 133;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels (
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133 133
133 AA; 16058 MW; 665E360246E9E3B0 CRC64;
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Yarol. 76:397-405(2002).

EMBI, AF45155; AAL66675.1; .

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0001998; F:structural molecule activity; IEA.

InterPro; IPR000328; Env_GP41.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VGBL_TaxID=11676;
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                                                                                     SEQUENCE FROM N.A.
                                   NCBI_TaxID=11676;
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Indels

99.3%; Score 138; DB 15; Length 133; 96.2%; Pred. No. 2.1e-13; 133 15794 MW; 9426B9B28EA26F6F CRC64; Query Match Best Local Similarity

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90MI60 RESULT 243 Q9IWQ6

1D ACC DDT ACC ACC DDT ACC DDT

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Ortiz M., Munoz L., Bernal A., Rodriguez A., Zorraquino A., Vadillo J., Salas A., Moreno A., Garcia-Saiz A.; Vadillo J., Salas A., Moreno A., Garcia-Saiz A.; Wadillo J., Salas A., Moreno A., Garcia-Saiz A.; Moreno E. M., Moreno E. Mon-B. HIV Type 1 Subtypes from Africa in Spain...; AIDS Res. Hum. Retroviruses 16:1967-1971(2000).

BMBL, PRESS918, AAG3893.1.; C.O. GO:0016021; C.integral to membrane; IEA.

GO: GO:0019031; C.viral envelope; IEA.

GO: GO:0005199; Fistructural molecule activity; IEA.

InterPro; IPRO00328; Env GP41.
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                                                                                                                                                                                                                                        Length 136;
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136 136
136 AA; 16415 MW; EP1069F332CF8128 CRC64;
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GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
VGBI_TaxID=11676;
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Pred. No. 2.2e-13;
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MEDLINE=20584646; PubMed=11153079;
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Best Local Similarity 96.2
Matches 25; Conservative
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Matches 25, Conservative
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X MEDLINE=1134754; PubMed=1124552;

A Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,

A Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,

Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;

T colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;

T from Kinshasa, Democratic Republic of Congo.";

AIDS Res. Hum. Retroviruses 17:361-365(2001).

R RGO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:00191; C:viral envelope; IEA.

R GO; GO:001931; C:viral envelope; IEA.

R GO; GO:001931; C:viral molecule activity; IEA.

R HoferPo; IPR000328; Env_GP41.
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99.3%; Score 138; DB 15; Length 134;
Best Local Similarity 96.2%; Pred. No. 2.1e-13;
Matches 25; Conservative 1; Mismatches 0; Indels (
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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J. Virol. 76:397-405(2002).
EMBL. AF405153; AAL66673.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
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Hum. Retroviruses 17:361-365(2001).
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STRAIN=85CD350;
MEDLINE=21134754;
Vang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
"Predominance of HIV type I subtype G among commercial sex workers from Kinshasa, Democratic Republic of Congo.";
Gonzalez Perez M.P., Garcia Saiz A.;
"Epidemiological and molecular characteristics of HIV and HTLV infection in Equatorial Guinea, 1996-1998.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF530021; AAP87752.1; -.
Envelope protein.
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"Epidemiological and molecular characteristics of HIV and HTLV infection in Equatorial Guinea, 1996-1998.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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140 AA; 16660 MW; 486490EA23F36A6A CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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EMBL, AF260483; AAF71950.1, ...
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001598; Fistructural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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143 AA; 17160 MW; D8157A905740B24E CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
VCBI_TaxID=11676;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein gp41 region (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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96.2%; Pred. No. 2.3e-13;
tive 1; Mismatches 0;
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MEDLINE=21134754; PubMed=11242522;
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MEDLINE=55251923; PubMed=7734184;
Calabro M.L., Zanotto C., Calderazzo F., Crivellaro C., Del Mistro A.,
De Rossi A., Chieco-Bianchi L.;
"HIV-1 infection of the thymus: evidence for a cytopathic and
thymotropic viral variant in vivo.";
AIDS Res. Hum. Retroviruses 11:11-19(1995).
EMBL; U09253; AAA79039.1; -.
GO; GO:0016011; C:integral to membrane; IEA.
GO; GO:0016011; C:integral to membrane; IEA.
GO; GO:0016013; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
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144 AA; 1727 MW; 233F7297E0E12C5B CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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NCBI_TaxID=11676;
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RESULT 252 Q7ZCE9

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STRAIN=HRLUX46-2;
STRAIN=HRLUX46-2;
Stown F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T., Stown T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
"Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naive patients infected with subtype B
and non-B HVV-1.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY185371; AA065646.1; --
GO; GO:0019931; C:vital envelope; IEA.
GO; GO:001998; Estructural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
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STRAIN=HRLUX50-1;
STRAIN=HRLUX50-1;
Staub T., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
"Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naive patients infected with subtype B
and non-B HIV-1.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY185378; AAO65653.1;
GO; GO:0019931; C:viral envelope; IEA.
GO; GO:001998; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41: 1.
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144 AA; 16770 MW; C3A3781F5BF13207 CRC64;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                             Viruses, Retroid viruses, Retroviridae, Lentivirus NCBL TaxID=11676,
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Pred. No. 2.3e-13;
1; Mismatches 0;
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Local Similarity 96.2%;
Les 25; Conservative
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Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
T. "Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naive patients infected with subtype B.
and non-B HIV-1.,
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY18330; AA065655.1; --
GO; GO:0019931; C:viral anvelope; IEA.
RO; GO:0005198; F:structural molecule activity; IEA.
Ro; GO:0005198; F:structural molecule activity; IEA.
Roy GO:000517; GP41; 1.
Roy Envelope protein.
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01-UTN-2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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1 RILAVERYLKDQQLLGIWGCSGKLIC 26
                              50 RVLAVERYLKDQQLLGIWGCSGKLIC 75
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hes 25; Conservative
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STRAIN=HRLUX50-2;
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EMBL, AV185382, AA065657.1; -. GO, GO:001931; C:viral envelope; IEA.

GO: GO:0005198; F:structural molecule activity; IEA.

InterPro: IPRO00328; Bnv GP41.

Emvelope protein.
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ROMAN F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
ROMAN F., Gonzalez D., Lambert C., Schneider F., Hemmer R., Schmit J.-C.;
Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naive patients infected with subtype B
and non-B HIV-1.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
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144 144
144 AA; 16795 MW; 5970F4D602702384 CRC64;
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144 AA; 16795 MW; 23E382827E63D165 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                          99.3%; Score 138; DB 15;
96.2%; Pred. No. 2.3e-13;
tive 1; Mismatches 0;
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                                                                                                   Best Local Similarity 96.28
Matches 25, Conservative
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nes 25; Conservative
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072CB8;
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01-JUN-2003
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Q7ZCB9
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Q7ZCB8
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99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels (
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EMBL; AY185394; AA065669.1; -.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0001918; F:structural molecule activity; IEA.
Har. PROOS17; GP41; 1.
Envelope protein.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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NCBL_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                 1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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SEQUENCE FROM N.A.
STRAIN=HRLUX59-2;
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SEQUENCE
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Best Local (
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Q7ZCC2
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Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T., Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.; Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.; "Uncommon mutations at residue positions critical for enfuvirtide (T-20) resistance in enfuvirtide-naive patients infected with subtype B and non-B HIV-1."; pto the EMBL/GenBank/DDBJ databases.

Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro: IPR000328; Env_GP41.

Envelope protein.
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EMBL, AY188401; AA065676.1; -...
GO; GO:001901198; F:structural molecule activity; IEA.

InterPro; IPR000328; Bnv_GP41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     144 AA; 16897 MW; 74BB5617D37F7468 CRC64;
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01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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Last sequence update)
Last annotation update)
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NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 138; DB 15;
Pred. No. 2.3e-13;
1; Mismatches 0;
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A Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
A Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
T. "Uncommon mutations at residue positions critical for entuvirtide (T-
AT 20) resistance in enfuvirtide-naive patients infected with subtype B
AS Staub HIV-1.";
And non-B HIV-1.";
ANIBBAGOS AAOGSOB1.1;
ANIBBAGOS AAOGSOB1.1;
ANIBBAGOS AAOGSOB1.1;
BENBL; AXIBBAGOS AAOGSOB1.1;
AC GO: GO: 0019031; C: viral envelope; IEA.
BR GO; GO: 0051993; Estructural molecule activity; IEA.
BR Fam; PF00517; GP41; 1.
BR Fam; PF00517; GP41; 1.
BR Fam; PR00517; GP41; 1.
BR Fam; PR00518; Extractural molecule activity; IEA.
BR Fam; PR00517; GP41; 1.
BR Fam; PR00518; Extractural molecule activity; IEA.
BR Fam; PR00518; Extractural molecule activity; IEA.
BR Fam; PR00517; GP41; 1.
BR Fam; PR00518; Extractural molecule activity; IEA.
BR Fam; PR00517; GP41; 1.
BR Fam; PR00518; Extractural molecule activity; IEA.
BR Fam; PR00517; GP41; 1.
BR Fam; PR00517; GP41; 1.
BR Fam; PR00518; Extractural molecule activity; IEA.
BR Fam; PR00517; GP41; 1.
BR Fam; PR00517; GP41; 1.
BR Fam; PR00518; Extractural molecule activity; IEA.
BR Fam; PR00518; Extractural molecule activity; 
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Submitted (Nov-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AY185409, AA065684.1;

GO; GO:0019919; F:structural molecule activity; IEA.

InterPro; IPR000328; Env. GP41:

Pfam; PF0017; GP41; 1.
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Local Similarity 96.2%; Pred. No. 2.3e-13;
es 25; Conservative 1; Mismatches 0; Indels 0
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144 AA; 16904 MW; C4E289C330AA4F41 CRC64;
                                                                                                         (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                               Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-QCT-2003 (TrEMBLrel. 25, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                  PRT;
                                                                                                                                                                                   Envelope glycoprotein (Fragment).
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                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                           [1] SEQUENCE FROM N.A.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                          STRAIN-HRLUX65-2;
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NON TER
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SEQUENCE 144 AA;
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01-JUN-2003
01-OCT-2003
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Q7ZCB4;
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               RESULT 263
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                                                                                                                                                                                   Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T., Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.; Uncommon mutations at residue positions critical for enfuvirtide (T-20) resistance in enfuvirtide-naive patients infected with subtype B and non-B HTV-1.", enfuvirtide-naive patients infected with subtype B Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

GO; GO:0019931; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GF41:
Envelope procein.
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99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels (
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NON_TER 144 144
SEQÜENCE 144 AA; 16951 MW; 99940DA637DA9D7F CRC64;
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144 AA; 16937 MW; 68F2D1D36DBF781B CRC64;
                                           Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Envelope glycoprotein (Fragment)
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Best Local Similarity 96.29
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Envelope protein.
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                      STRAIN=HRLUX63-2;
                                                                                              NCBI_TaxID=11676;
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144
16701 MW; 40FFEFCF6BBF14F4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus
                                                                                                                                Query Match
Best Local Similarity 96.2%;
Matches 25; Conservative
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                                                                                144 AA;
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Envelope protein.
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Q7ZCA5,
01-JUN-2003
01-JUN-2003
                                                NON_TER
SEQUENCE
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Q72C98;
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072C98
AC 072C98
DT 01-JUN
DT 01-JUN
DT 01-JUN
DT 01-CT
DE ENV-10
CO VITUSE
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Q7ZCAS
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Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
"Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naive patients infected with subtype B
and non-B HIV-1.";
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  Indels
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0003198; F:structural molecule activity; IEA.
Intervo: IPRO0328; Env_GP41.
                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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1; Mismatches
                                                   1 RILAVERYLKDQQLLGIWGCSGKLIC 26
                                                                                50 RVLAVERYLKDQQLLGIWGCSGKLIC 75
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Conservative
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Q7ZCB0;
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Q7ZCA6
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Q7ZCB0
Matches
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Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T., Staub T., Staub T., Schmit J.-C.; Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.; Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.; John Common mutations ar residue positions critical for enfuvirtide (T-20) resistance in enfuvirtide-naive patients infected with subtype B and non-B HIV-1."; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases. EMBL; Ax188415; Ax058590.1; -GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000328; Enructural molecule activity; IEA.
PFem; PP00517; GP41; 1.
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Length 144;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Score 138; DB 15; 1
Pred. No. 2.3e-13;
1; Mismatches 0;
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Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T., Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.; "Uncommon mutations at residue positions critical for enfuvirtide (T-20) resistance in enfuvirtide-naive patients infected with subtype B and non-B HIV-1."; Bubly fendank/DDBJ databases.

Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

GO; GO:001931; C:viral envelope; IEA.

GO; GO:001981; P:structural molecule activity; IEA.

First. PR000328; Env. GP41:
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99.3%; Score 138; DB 15; Length 144;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0
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144 AA; 16856 MW; E89941A2A9E2F16C CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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NCBI_TaxID=11676;
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01-JUN-2003 (TrEMBLrel. 24, Created)
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1es 25; Conservative
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SEQUENCE FROM N.A.
STRAIN=HRLUX89-1;
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Q7ZC71
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Q7ZC70
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AC Q7ZC70
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STRAIN=HRLUX75-1;
STRAIN=HRLUX75-1;
Stoman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Staub T., Boulme R., Arendt V., Schneider F., Henmer R., Schnit J.-C.,
"Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naive patients infected with subtype B
and non-B HIV-1.";
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and non-B HIV-1."; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases. Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AY189422; AA0656971; -. GO; GO:001931; C:viral envelope; IEA. GO; GO:0005198; F:structural molecule activity; IEA. InterPro; IPR000228; Env GP41. Pfam; PF00517; GP41; 1. Envelope protein.
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EMBL; AY185424; AAO65699.1; -.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005199; F:structural molecule activity; IEA.
InterPro; IRR0000229; Env. GP41.
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144 AA; 16877 MW; 619841A2A7D5ECD4 CRC64;
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01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VGH_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Best Local Similarity 96.2*
Matches 25; Conservative
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Q72C49;
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Q7ZC49
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
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144 Aa; 16810 MW; E811A60B17491895 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                               Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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                                        Envelope glycoprotein (Fragment).
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Matches 25; Conservative
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Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T., Staub T., Boulme R., Akendt V., Schneider F., Hemmer R., Schmit J.-C.; "Uncommon mutations at residue positions critical for enfuvirtide (T-20) resistance in enfuvirtide-naive patients infected with B and non-B
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
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17033 MW; F899F94713F5D4D0 CRC64;
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GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; ENV GP41.
PF00517; GP41; 1.
                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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1 Similarity 96.2%;
25; Conservative :
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PRELIMINARY;
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Best Local Similarity
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Length 145;

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Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T., Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C., "Uncommon mutations at residue positions critical for enfuvirtide (T-20) resistance in enfuvirtide-naive patients infected with B and non-B
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Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subtype HIV-1.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AX185452; Ax18452.1;
GO, GO:001991; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
Envelope protein.
                                                                                                                                          145 AA; 17043 MW; 4487A149CEC57570 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                             99.3%; Score 138; DB 15; 96.2%; Pred. No. 2.3e-13; 1ive 1; Mismatches 0;
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                InterPro; IPR000328; Env GP41.
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Matches 25; Conservative
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Best Local Similarity 96.2<sup>§</sup>
Matches 25, Conservative
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                                   Pfam; PF00517; GP41; 1.
Envelope protein.
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SEQUENCE
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Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naive patients infected with B and non-B
subtype HIV-1.";
Subrited (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, A1185488, AA065763.1;
GO; GO: GO: GO: GO: Coviral envelope; IEA.
GO; GO: GO: S198; F: Structural molecule activity; IEA.
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99.3%; Score 138; DB 15; Length 145; 96.2%; Pred. No. 2.3e-13; ive 1; Mismatches 0; Indels 0
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                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subtype HIV-1.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX188-487; AA065762.1;
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IRR00328; Env. GP41.
Pfam; PF00517; GP41; 1.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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                                                   25; Conservative
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                  Best Local Similarity
Matches 25; Conserv
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Query Match
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Q7ZC33;
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MEDINE-22092513; PubMed-12097573;

MEDINE-22092513; PubMed-12097573;

MEDINE-22092513; PubMed-12097573;

Boutonnet N., Janssens W., Boutton C., Verschelde J.L., Heyndrickx L.,

Beirnaert E., van der Groen G., Lasters I.;

"Comparison of predicted scaffold-compatible sequence variation in the
triple-hairpin structure of human immunodeficiency virus type 1 gp41

"vith patient data.";

J. Virol. 76:7595-7666(2002).

REMBL; AJ428020; CAD20972.1;

RO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:integral to membrane; IEA.

RO; GO:0019031; C:viral envelope; IEA.

RO; GO:0005198; F:structural molecule activity; IEA.

REMBL: PF00517; GP41; 1.
      "Epidemiological and molecular characteristics of HIV and linfection in Equatorial Guinea, 1996-1998."; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AFS29972; AAP87703.1; -.
                                                                                                                                                                                                                          147 AA; 17548 MW; 8F5E56215D1D1682 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                    99.3%; Score 138; DB 15; 96.2%; Pred. No. 2.3e-13; live 1; Mismatches 0;
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SEQUENCE FROM N.A.
MEDLINE=22092513; PubMed=12097573;
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Matches 25; Conservative
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"Uncommon mutations at residue positions critical for enfuvirtide (T-
20) resistance in enfuvirtide-naive patients infected with B and non-B
subtype HIV-1.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY185490; AA065765.1; -.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR000328; Env GP41.
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EMBL, AF529979; AAP87710.1; -.
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99.3%; Score 138; DB 15; Length 146;
Best Local Similarity 96.2%; Pred. No. 2.3e-13;
Matches 25; Conservative 1; Mismatches 0; Indels
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Envelope glycoprotein (Fragment).
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Matches 25; Conservative
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Q7SM44
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Human immunodeficiency virus 1.
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                  Beirnaert E., van der Groen G., Lasters I., "Comparison of predicted scaffold-compatible sequence variation in the triple-hairpin structure of human immunodeficiency virus type 1 gp41
        Verschelde J.L., Heyndrickx L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High frequency of recombinant genomes in HIV-1 samples from Brazilian
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Morgado M.G.;
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96.2%; Pred. No. 2.5e-13;
Live 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                          155 155
155 AA; 18273 MW; B4EBAC6F0C278B2F CRC64;
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                                                                             with patient data.";

'Virol. 76:7595-7606(2002).

EMBL; AJ428002; CAD20954.1; -

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro: IPR000328; Env_GP41.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Last annotation update)
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Boutonnet N., Janssens W., Boutton C.,
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Q8J3Q9,
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01-OCT-2002 (TEMBLEEL, 22,
01-UNN-2003 (TEMBLEEL, 24,
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Best Local Similarity 96.2<sup>3</sup>
Matches 25; Conservative
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PSECURACE FROM N.A.

REDLINE-22092513; PubMed=12097573;

A MEDLINE-22092513; PubMed=12097573;

A Boutonnet N., Janssens W., Boutton C., Verschelde J.L., Heyndrickx L.,

A Boutonnet E., van der Groen G., Lasters I.;

T "Comparison of predicted scaffold-compatible sequence variation in the stringle-hairpin structure of human immunodeficiency virus type 1 gp41

XT triple-hairpin structure of human immunodeficiency virus type 1 gp41

XT triple-hairpin structure of human immunodeficiency virus type 1 gp41

XT virol. 76:7595-7606(2002).

DR GO: GO:0016021; C:integral to membrane; IEA.

GO: GO:0016021; C:integral to membrane; IEA.

GO: GO:0016021; C:integral to membrane; IEA.

GO: GO:0010911; C:integral to membrane; IEA.

RO: GO:0001981; F:structural molecule activity; IEA.

InterPro: IPR000328; Env_GP41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.3%; Score 138; DB 15; Length 156; 96.2%; Pred. No. 2.5e-13; tive 1; Mismatches 0; Indels 0
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
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156 AA; 18491 MW; 54BFBB0BC6FB76DD CRC64;
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19242 MW; C580C6B44534772E CRC64;
Viruses, Retroid viruses; Retroviridae, Lentivirus.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNS-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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51 RVLAVERYLKDQQLLGIWGCSGKLIC 76

163 AA.

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Feng H., Huang Y., Yang D., Tang H., Hu X.; "Phylogenetic analysis of part of env gene of HIV-1 isolates from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 163;
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY0379533, AAK72336.1; -.
GO; GO:0016021; C:inregral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPror; IPR000328; Env_GP41.
Transmembrane.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Pred. No. 2.6e-13;
1; Mismatches 0;
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Q90E67
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                                                                                                                                                                                                                                                              Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AV039954; ANK72377.1; -. EMBL, ANK73277.1; -. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0019031; C:viral envelope; IEA. GO; GO:0005198; F:structural molecule activity; IEA. InterPro; IPR00328; Env_GP41.
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163 AA; 19285 MW; 2B9917C07613DIFE CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19; Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                         Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Best Local Similarity 96.2*
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                                                                                                                                                                    SEQUENCE FROM N.A.
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Feng H., Huang Y., Yang D., Tang H., Hu X.; "Phylogenetic analysis of part of env gene of HIV-1 isolates from
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                                                                                       Length 163;
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163 163
163 AA; 19311 MW; F325C8FD7143D237 CRC64;
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EMBL; AX037958; AAK72331.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
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163 AA; 19347 MW; C397BBBE5624A725 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Feng H., Huang Y., Yang D., Tang H., Hu X.;
"Phylogenetic analysis of part of env gene of HIV-1 isolates from
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                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AV037962; ARV72335.1; -...
GO; GO:0016C31; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IRR000328; Env_GP41: 1.
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AX037959; AAK72321; -.
GO; GO:0016031; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
Interpreto; IPR000328; Env GP41.
Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 163
163 AA; 19200 MW; EF4E811ED3871087 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                        Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
. 2.6e-13; .
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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             Pred. No. 2.66
1; Mismatches
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                                                                                1 RILAVERYLKDQQLLGIWGCSGKLIC 26
                                                          1 RILAVERYLKDOQLLGIWGCSGKLIC
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          96.2%;
          Best Local Similarity 96.24
Matches 25; Conservative
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Best Local Similarity 96.2%
Warches 25; Conservative
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01-DEC-2001
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Q90E71 RESULT 292

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Length 164;

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Beirnaert E., van der Groen G., Lasters I.;
"Comparison of predicted scaffold-compatible sequence variation in the
triple-hairpin structure of human immunodeficiency virus type 1 gp41
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164 AA; 19291 MW; F91298D132E359C7 CRC64;
                                                                                                                        J. Virol. 76:7595-7606(2002).

EMBL; AJ427991; CAD50943.1.

EMBL; AJ427991; CAD50943.1.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:00190318; F:structural molecule activity; IEA.

InterPro: IPR00517; GP41: 1.
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Best Local Similarity 96.24
Matches 25; Conservative
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SEQUENCE FROM N.A.
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01-JUN-2003
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Q90E78
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MEDLINE=22092513; PubMed=12097573;
Boutonnet N., Janssens W., Boutton C., Verschelde J.L., Heyndrickx L.,
                                                                                                                                                                                                                                                                                                                                         Gaps
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                 163 AA; 19370 MW; 82180C09173ADCA8 CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                            InterPro; IPR000328; Env GP41.
Pfam; PF00517; GP41; 1.
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Pfam; PF00517; GP41; 1.
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Matches 25; Conservative
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Q8J3R2;
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164 AA; 19224 MW; 078AD292ED08AC4F CRC64;
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databai
EMBL, AY037952; AAK72325.1; -
GO; GO:001601; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
                                                                                                                                                                                         (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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NCBL_TaxID=11676;
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Pred. No. 2.6e-13;
1; Mismatches 0;
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1 RILAVERYLKDOQLLGIWGCSGKLIC 26
                        1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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Feng H., Huang Y., Yang D., Tang H., Hu X., "Phylogenetic analysis of part of env gene of HIV-1 isolates from
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                                                                                                                                                                                                                                                                                                                                       164 164
164 AA; 19249 MW; 4218E2E1AF2150EF CRC64;
         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNI-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                              Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                            NCBI_TaxID=11676;
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                                                                                 Feng H., Huang Y., Yang D., Tang H., Hu X.;
"Phylogenetic analysis of part of env gene of HIV-1 isolates from Suchuan.",
Submitted (UUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY037949; AAK72122.1; -.
GO; GO:0015021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41; 1.
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Feng H., Huang Y., Yang D., Tang H., Hu X.;
"Phylogenetic analysis of part of env gene of HIV-1 isolates from
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99.3%; Score 138; DB 15; Length 164;
Best Local Similarity 96.2%; Pred. No. 2.6e-13;
Matches 25; Conservative 1; Mismatches 0; Indels (
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY037966; AAK72339.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019931; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
Interbro; IRR000328; Env_GP41.
PFam; PF00517; GP41; 1.
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164 AA; 19272 MW; CC3567E17D3D322E CRC64;
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19389 MW; 505315DE3C2E2D87 CRC64;
               Retroid viruses; Retroviridae; Lentivirus.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 AA
                                                                                                                                                                                                                                                                                                                                                            1 RILAVERYLKDOOLLGIWGCSGKLIC 26
                                                                                                                                                                                                                                                                                                                                                                                 52 RVLAVERYLKDQQLLGIWGCSGKLIC 77
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Human immunodeficiency virus 1.
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es 25; Conserv
                                                       SEQUENCE FROM N.A.
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SEQUENCE
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Q90E70
ID Q90E70
AC Q90E70
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cch 99.3%; Score 138; DB 15; Length 164; al Similarity 96.2%; Pred. No. 2.6e-13; 25; Conservative 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 99.3%; Score 138; DB 15; Length 164; l Similarity 96.2%; Pred. No. 2.6e-13; 25; Conservative 1; Mismatches 0; Indels
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
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164 AA; 19246 MW; 0FC57937F2165F31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AY031948; AAK72321.1; -... GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0019031; C:viral envelope; IEA. III. InterPro; IPR000328; Exructural molecule activity; IEA. Pfam; PF00517; GP41; 1.
                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                               164 AA.
                                                                                              1 RILAVERYLKDQQLLGIWGCSGKLIC 26
                                                                                                                           52 RVLAVERYLKDQQLLGIWGCSGKLIC 77
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                        Local Similarity
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Best Local Similarity
Matches 25; Conserv
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164 AA

PRT;

PRELIMINARY;

Q90E70 Q90E70;

188 AA

QBJERS

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"High frequency of recombinant genomes in HIV-1 samples from Brazilian Southeastern and Southern regions.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF463486; AM490812.1;
CO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:005931; C:viral envelope; IEA.

InterPro; IPR000328; Env GP41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
Morgado M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 AA; 21441 MW; 80D9C61680E67E35 CRC64;
                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Bnvelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
51 RVLAVERYLKDQQLLGIWGCSGKLIC 76
                                                                                                                                                                          PRT;
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Best Local Similarity 96.2%;
Matches 25; Conservative
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Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
                                                                                                                                                                          PRELIMINARY;
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SEQUENCE FROM N.A.
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01-JUN-2003
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SEQUENCE
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Q8JAJ7
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Q8JAK8
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Poveda E., Rodes B., Toro C., Martin-Carbonero L., Soriano V.;
"Evolution of the env gene (gp41) in HIV-1 positive patients receiving
T-20, a fusion inhibitor.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF500087; AAM21673.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR00028; Env GP41.
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Poveda E., Rodes B., Toro C., Martin-Carbonero L., Soriano V.;
"Evolution of the env gene (gp41) in HIV-1 positive patients receiving the fusion inhibitor.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AFS00086; AAM21672.1;
GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001991; C:viral envelope; IEA.

InterPro; IPR000328; Env GP41.

Pfam; PF00517; GP41; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.3%; Score 138; DB 15; Length 180; Best Local Similarity 96.2%; Pred. No. 2.9e-13; Matches 25; Conservative 1; Mismatches 0; Indels (
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181 AA; 21126 MW; 27DF2E95E885C2AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 AA; 21017 MW; 5C1AEE2C3D95AA49 CRC64;
                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                     Viruses; Retroid viruses; Retroviridae; Lentivirus
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Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                      180 AA.
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                                                                                      PRT;
                                                                                                                                                                                                                             Envelope glycoprotein (Fragment).
Human immunodeficiency virus 1.
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Best Local Similarity 96.21
Matches 25; Conservative
                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=11676;
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QBJER4;
                                                                                   Q8JER3
                             RESULT 302
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Q8JER

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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF463447; AAM90823.1, comparing to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0006198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
                                                                Gaps
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        Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
Morgado M.G.;
                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
Score 138; DB 15;
Pred. No. 3e-13;
                                                                                                                                                                                                                                                                                                                    190 AA
                                                             1; Mismatches
                                                                                                                                                       1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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RT and trequency of recombinant genomes in HIV-1 samples from Brazilian RT Southeastern and Southern regions.";

Sutheastern and Southern regions.";

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

BR SMBL, AF46131; AAM90807.1; -.

BR GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral cappid; IEA.

BR GO; GO:0019038; C:viral envelope; IEA.

BR GO; GO:0019038; Envelope; IEA.

BR GO; GO:0019038; Envelope; IEA.

BR GO; GO:005198; F:structural molecule activity; IEA.

BR HOREPRO; IPR000777; GP41.

BR Ffam; PP00516; GP120; 1.

BR Ffam; PP00516; GP120; 1.

BR Ffam; PR00517; GP41; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 138; DB 15; Length 199;
Pred. No. 3.2e-13;
1; Mismatches 0; Indels (
                                                                             Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
Morgado M.G.;
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Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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les 25; Conservative
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201 AA;
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Q8JAL5
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Southeastern and Southern regions.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF463432; AmM90808.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capaid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000128; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00514; GP120; 1.
Pfam; PF00517; GP41; 1.
ALDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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                         Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
                                                                                                                                                                                                                                                                               Score 138; DB 15; Length 190;
Pred. No. 3.1e-13;
1; Mismatches 0; Indels (
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Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
Morgado M.G.;
                                                                                                                                                                        190 190
190 Aa; 21717 MW; BDA818CAB5A8329F CRC64;
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192 AA; 22182 MW; 357E8C354BD97D1A CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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InterPro; IPR000777; GP120.
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Best Local Similarity 96.28
Matches 25; Conservative
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Best Local Similarity 96.2%
Matches 25, Conservative
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InterPro; IPR00077; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41: 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 99.3%; Score 138; DB 15; Length 201; 1 Similarity 96.2%; Pred. No. 3.3e-13; 25; Conservative 1; Mismatches 0; Indels 0
Southeastern and Southern regions.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF463429; AAM90805.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:irral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:Structural molecule activity; IEA.
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01-JUN-2001
01-JUN-2001
01-JUN-2003
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01-JUN-2003
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STRAIN=95BRRJ011;
Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
Morgado M.G.;
"High frequency of recombinant genomes in HIV-1 samples from Brazilian
Southeastern and Southern regions.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF465424; AAM90800.1;
SOUGO GO: GO: Colorogic C: viral cappid; IEA.

GO; GO: 0015028; C: viral cappid; IEA.

GO; GO: 0019031; C: viral envelope; IEA.

GO; GO: 0019031; C: viral envelope; IEA.

RO; GO: 0019031; C: viral envelope; IEA.

RO; GO: 0019031; G: viral envelope; IEA.
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=95BRRJ013;
Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
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201 AA; 23281 MW; 67ABC2E7D2C93E44 CRC64;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; ENV GP41.
                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBL_TaxID=11676;
                                                                                                                             201 AA
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                                                                                                                             PRT;
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                                                                                                                    PRELIMINARY;
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01-OCT-2002
01-OCT-2002
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                                RESULT 309
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Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,
Zivny I., Jarry W., Pozzi L., Kurane I., Ennis F.;
"Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established
at two different time points: Role of CTL in the emergence of escaped
mutants.";
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,
Zivny I., Jarry W., Pozzi L., Kurane I., Ennis F.;
"Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established
at two different time points: Role of CTL in the emergence of escaped
mutants.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB047357; BAB32638.1; -.
                                                                                                                                                                             Gaps
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AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.

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NON TER 217 217

SEQÜENCE 217 AA; 24952 MW; 3F41BA3210A46167 CRC64;
                                                                                                                         Length 217;
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                                                                                                                                                                             0; Indels
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IRR000328; Env GP41.
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NCBI_TaxID=11676;
                                                                                                                   ch 99.3%; Score 138; DB 15; 1 Similarity 96.2%; Pred. No. 3.5e-13; 25; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 138; DB 15;
Pred. No. 3.7e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 17, Created)
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illarity 96.2%;
Conservative
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NON TER 225 225
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Best Local Similarity
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es 25; Conserv
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Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J., Zivny I., Jarry W., Pozzi L., Kurane I., Ennis F.; "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established at two different time points: Role of CTL in the emergence of escaped
                                       at two different time points: Role of CTL in the emergence of escaped
         "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established
                                                                                                                                                                                                                                                                                                                                                                                                                                                99.3%; Score 138; DB 15; Length 225; 96.2%; Pred. No. 3.7e-13; ive 1; Mismatches 0; Indels C
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                                                                                  EMBL; AB047353; BAB35634.1; -...

EMBL; AB047353; BAB35634.1; -...

GO, GO:0016621; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:001998; F:structural molecule activity; IEA.

InterPro; IPR000228; Bnv GP41.

Polyprotein; Transmembrane.

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SEQÜENCE 225 AA; 25609 MW; 6C1A3A0334931031 CRC64;
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GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0019031; C:viral envelope; IEA.
GO, GO:0005198; F:structural molecule activity; IEA.
InterPro; IRR00328; Env_GP41.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope polyprotein (Fragment).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope polyprotein (Fragment).
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
VGI_TaxID=11676;
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Best Local Similarity 96.2<sup>§</sup>
Matches 25, Conservative
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nes 25; Conservative
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ID Q99IC5
AC Q99IC5;
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Matches
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Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,
Zivny I., Jarry W., Pozzi L., Kurane I., Ennis F.;
"Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established
at two different time points: Role of CTL in the emergence of escaped
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Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J.,
Zivny I., Jarry W., Pozzi L., Kurane I., Ennis F.;
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99.3%; Score 138; DB 15; Length 225;
Best Local Similarity 96.2%; Pred. No. 3.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                         225
25557 MW; C5660AE8589DDFA6 CRC64;
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25480 MW; C2166441900478ED CRC64;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IFR000328; Env_GP41.
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Envelope polyprotein (Fragment).
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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NCBI_TaxID=11676;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  1 RILAVERYLKDOQLLGIWGCSGKLIC 26
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Human immunodeficiency virus 1.
                                                                                                                Pfam; PF00517; GP41; 1.
Polyprotein; Transmembrane.
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                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 96.23
Matches 25, Conservative
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225 AA;
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225 AA;
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SEQUENCE
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MEDINE=92144209; PubMed=1736940; Steuler H., Storch-Hagenlocher B., Wildemann B.; Steuler H., Storch-Hagenlocher B., Wildemann B.; Steuler Propulations of Human immunodeficiency virus type 1 in blood and cerebrospinal fluid."
ALIOS Res. Hum. Retroviruses 8:53-59(1992).
EMBL, X61358; CAA43628.1; --
PIR; S70424; S21992.
                                                                                                                                                                                           Steller H., Storch-Hagenlocher B., Wildemann B.; "Distinct populations of Human immunodeficiency virus type 1 in blood and cerebrospinal fluid.";
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357 AA; 41248 MW; C3E22F3EF8C4847E CRC64;
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EMBL, X61354; CAA43620.1; -.

PIR; A53591 A53591.

PIR; A70420; S22006.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:005199; F:etructural molecule activity; IEA.
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005199; F:etructural molecule activity; IEA.
Pfam; PF00517; GP41; 1.
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope protein, gp120/gp41 (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                           Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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96.2%; Pred. No. 5.9e-13;
iive 1; Mismatches 0;
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                                    Envelope protein, gp120 /gp41 (Fragment)
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                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=92144209; PubMed=1736940;
                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000328; Env_GP41.
Pfam; PF00517; GP41; 1.
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es 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane.
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SEQÜENCE
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EMBL; X61355; CAA43622.1; -.
                                                       Ishiko H., West K., Zeng W., Spaulding A., Islam S., Norman J., Zivny I., Jarry W., Pozzi L., Kurane I., Ennis F.; "Autologous HIV-1-specific cytotoxic T lymphocytes (CTL) established at two different time points: Role of CTL in the emergence of escaped
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             99.3%; Score 138; DB 15; Length 225; 96.2%; Pred. No. 3.7e-13;
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                                                                                                                                mutants.";
submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB047356; BAB32637.1;
GQ; GQ:001021; C:integral to membrane; IEA.
GQ; GO:0019031; C:viral envelope; IEA.
GQ; GO:005198; F:structural molecule activity; IEA.
InterProf. IPRO.00328; Env.GP41.
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                                                                                                                                                                                                                                                                                                                                                    225 AA; 25579 MW; B9013F57411CDDCB CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope protein, 9p120 /9p41 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676,
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                                                                                                                                                                                                                                                                                                 Polyprotein; Transmembrane.
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les 25; Conservative
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                                    SEQUENCE FROM N.A.
  NCBI_TaxID=11676;
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Q8QDX2
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Q8QE11
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JONASSEN T.O., Grinde B., ABJO B., Hasle G., Hungnes O.;
"Inter-subtype recombinant HIV-1 involving HIV-MAL-like and subtype H-
like sequence in four Norwegian cases ";
AIDS Res. Hum. Retroviruses 16:49-58(2000).
BMB.; AJ237569; CAB19745.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0015198; F:structural molecule activity; IEA.
InterPro; IPR000328; ENV GP41.
                                                                                                                                                         MEDLINE=92144209; PubMed=1736940;
Steallar H., Storch-Hagenlocher B., Wildemann B.;
"Distinct populations of Human immunodeficiency virus type 1 in blood
and cerebrospinal fluid.";
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                  Length 357;
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                          357 AA; 41152 MW; 07462A9B4505C734 CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env_GP41.
                                                           Last sequence update)
Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Gp41 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                   Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                           357 AA.
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                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                  AIDS Res. Hum. Retroviruses 8:53-59(1992).
ERBL; X61353; CAA43618.1; -.
PIR; A53591; A33591.
PIR; S22004; S22004.
                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequenc
01-JUN-2003 (TrEMBLrel. 24, Last annotat
Envelope protein, gpl20 /gp41 (Fragment)
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MEDLINE=20092438; PubMed=10628816;
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Best Local Similarity 96.2*
Matches 25; Conservative
                         PRELIMINARY;
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Pfam; PF00517; GP41; 1.
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SEQUENCE
                                   078155;
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Q9WIT0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-SQUAD116;
Masharsky A.E., Eremin V.F., Kozlov A.P.;
Machar cloning and analysis of full-length human immunodeficiency virus type 1 genomes of prevalent strains among IDUs in countries of the FSU.",
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF413981; AAL78436.1; -.
                                                     Gaps
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AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
  Length 362;
                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the FSU.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AP414005, AAL78485.1;
GO, GO:0019028; C:integral to membrane; IEA.
GO, GO:0019028; C:viral capsid; IEA.
GO, GO:0019031; C:viral envelope; IEA.
GO, GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Bny GP41.
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                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
  DB 15;
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96.2%; Pred. No. 6.3e-13;
iive 1; Mismatches 0;
99.3%; Score 138; DB 15
96.2%; Pred. No. 6e-13;
live 1; Mismatches
                                                                                                                                                                                                                                                                                     380 AA
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                                                                                                      1 RILAVERYLKDQQLLGIWGCSGKLIC
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nes 25; Conservative
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Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
Morgado M.G.;
"High Frequency of Recombinant Genomes in HIV-1 Samples From Brazilian
                                                                                                                                Masharsky A.E., Bremin V.F., Kozlov A.P., Moslov A.P., Molecular cloning and analysis of full-length human immunodeficiency virus type 1 genomes of prevalent strains among IDUs in countries of the FSU.";
                                                                                                                                                                                                                                                                                                     EMBL; AF413982; AAL78438.1; -. GO; GO: 0016021; C: integral to membrane; IBA. GO; GO: 0016021; C: integral to membrane; IBA. GO; GO: 0019028; C: viral capsid; IBA. GO; GO: 0019031; C: viral envelope; IBA. GO; GO: 0019031; F: structural molecule activity; IBA. InterPro; IPR000328; Env GP41. InterPro; IPR000777; GP120. Ffam; PF00516; GP120; 1. Pfam; PF00516; GP120; 1. AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; AV072000; AAL62003.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:005198; P:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
                                                                                                                                                                                                                                                                               Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 AA; 44020 MW; 4E58E7273CA1E050 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
            Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Best Local Similarity 96.2
Matches 25; Conservative
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Pfam; PF00517; GP41; 1
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                                        NCBI_TaxID=11676;
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"Molecular cloning and analysis of full-length human immunodeficiency virus type I genomes of prevalent strains among IDUs in countries of the FSU.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR00077; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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PF00517; GP41; 1.
Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                    99.3%; Score 138; DB 15; Length 387; 96.2%; Pred. No. 6.4e-13;
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral capsid; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IPR000328; EN GP41.

InterPro; IPR000777; GP120.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Matches 25; Conservative
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Q8QE07;
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RESULT 325 Q8QE07

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Q8QE15 RESULT 324 Q8QE15

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Length 392;

072603; 072603

RESULT 327 072603

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305 RVLAVERYLKDQQLLGIWGCSGKLIC 330
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Pfam; PF00517; GP41; 1.
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"High frequency of HIV-1 recombinant genomes in samples from southeast and south regions of Brazil.";

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF062424; AAC17163.2; - EMBL/GenBank DDBJ databases.

EMBL; AF062424; AAC17163.2; - EMBL/GenBank DDBJ databases.

GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IPR000328; Env GP41.
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                                                                                01-AUG-1998 (TrEMBLrel. 07, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                         Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                      398 AA.
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                                                      PRT;
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STRAIN=95BRRJ014;
MEDLINE=20199695; PubMed=10737434;
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STRAIN-95BRSP004;
MEDLINE-20199695; PubMed=10737434;
                                                                                                                               Envelope glycoprotein (Fragment).
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                                                     PRELIMINARY;
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Pfam; PF00517; GP41; 1.
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Query Match

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"High Frequency of Recombinant Genomes in HIV-1 Samples From Brazilian Strange From Strange Southearn and Southern Regions."; Southeastern and Southern Regions."; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; ANO71998; AAL62001.1; -.

REMBL; ANO71998; AAL62001.1; -.

RO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:iviral envelope; IEA.

GO; GO:0019031; C:iviral envelope; IEA.

GO; GO:0019031; C:iviral envelope; IEA.

RO; GO:0019031; C:iviral envelope; IEA.

RO; GO:0019031; C:iviral envelope; IEA.

RO; GO:0019031; GP10.

RITHERPO; IPRO00777; GP120.

REfam; PF00516; GP120; 1.

REfam; PF00516; GP120; 1.

RAIDS; Coat protein; GP41; 1.

RAIDS; Coat protein; Glycoprotein; Transmembrane.

TONN TER 416 416
Bongertz V., Bou-Habib D.C., Brigido L.F.M., Caseiro M., Chequer P.J., Couto-Fernandez J.C., Ferreira P.C., Galvao-Castro B., Greco D., Guimaraes M.L., Linhares de Carvalho M.I., Morgado M.G., Oliveira C.A., Osmanov S., Ramos C.A., Rossini M., Sabino E., Tanuri A., Ueda M.; Razil: genetic, biologic, and immunologic characterization of HIV-1 strains in three potential HIV vaccine evaluation sites. Brazilian Network for HIV Isolation and Characterization."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guimaraes M.;
"High frequency of HIV-1 recombinant genomes in samples from southeast and south regions of Brazil.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF062423; AAC17162.2; -.
PIR; A53591; A53591.
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Pred. No. 6.9e-13;
1; Mismatches 0; Indels 0
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Morgado M.G.;
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416 AA; 47011 MW; 3E6244DFAC4A8703 CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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Gaps

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Length 546;

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"env gene sequences of primary HIV type 1 isolates of subtypes B, C, D, E, and F obtained from the World Health Organization Network for HIV Isolation and Characterization.";
AIDS Ree. Hum. Retroviruses 12:741-747(1996).

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0019038; F:structural molecule activity; IEA.

InterPro; IPR000128; Env GP41.
McWilliams N., Trkola A., Moore J.P., Wolinsky S.M.;
"Immunological and virological analyses of persons infected by
immunodeficiency virus type 1 while participating in trials of
recombinant gpl20 subunit vaccines.";
J. Virol. 72:1552-1876(1998).
EMBL; U84885; AAC58931.1;
                                                                        EMBL; U84885; AAC58931.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IRR000328; Env GP41.
InterPro; IRR000777; GP120.
Pfam; PP00516; GP120; 1.
Pfam; PF00517; GP41; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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MEDLINE=96303593; PubMed=8744585;
Penny M.A., Thomas S.J., Douglas N.W., Ranjbar S., Holmes H.,
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AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane. errimence 605 AA; 67420 MW; B384ACADAISAE6FB CRC64;
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Pred. No. 1e-12;
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Pred. No. 9.2e-13;
1; Mismatches 0; Indels
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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Best Local Similarity 96.2%;
Matches 25; Conservative
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Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Envelope glycoprotein.
                                                                                                                                                                                                                                                  546 AA;
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Daniels R.S.;
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Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,
Walker B.D., Neumann A.U., Vermund S.H., Mestecky J., Jackson S.,
Fenamore E., Cao Y., Gao F., Kalams S., Kunstman K.J., McDonald D.,
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
                            Query Match 99.3%; Score 138; DB 15; Length 416; Best Local Similarity 96.2%; Pred. No. 6.9e-13; Matches 25; Conservative 1; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                        Guimaraes M.L., Moreira A.S., Loureiro R., Galvao-Castro B.,
Morgado M.G.;
 416 AA; 47011 MW; 3E6244DFAC4A8703 CRC64;
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                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                    Viruses, Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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NCBI_TaxID=11676;
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96.2%; Pred. No. 7e-13;
live 1; Mismatches
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                                                                                     1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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les 25, Conservative
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STRAIN=96BRRJ101;
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STRAIN=546hc-F7;
Gartner S., Liu Y., Tang X.P., McArthur J.C., Scott J.;
Gartner S., Liu Y., Tang X.P., McArthur J.C., Scott J.;
Manalysis of human immunodeficiency virus type 1 gp160 sequences from a patient with HIV dementia: evidence for monocyte trafficking into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=546hc-B6;
Gartner S., Liu Y., Tang X.P., McArthur J.C., Scott J.;
"Analysis of human immunodeficiency virus type 1 gp160 sequences from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
  Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 616 AA; 68756 WW; BES5DARSBAS9EC15 CRC64;
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EMBL, APC7116; AAF75507.1; -
GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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NCBL TaxID=11676;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                 Score 138; DB 15;
Pred. No. 1e-12;
1; Mismatches 0;
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                                                                                                   99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 brain.";
J. Neurovirol. 0:0-0(2000)
                                                                                                                                          25; Conservative
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Pfam; PF00517; GP41; 1.
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Best Local Similarity
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SEQUENCE FROM N.A.
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                                          AIDS; Coa
SEQUENCE
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MEDLINE=20386756; PubMed=10933619;
Liitsola K., Holm K., Bobkov A., Pokrovski V., Smolskaja T.,
Leinikki P., Osmanov S., Salminen M., UNAIDS Virus Isolation Network;
"An AB recombinant and its parental HIV type 1 strains in the area of
the former soviet union: low requirements for sequence identity in
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Daniels R.S., Patel D., Xiang Z., Zheng N.N., Kang C.;
Daniels R.S., Patel D., Xiang Z., Zheng N.N., Kang C.;
"Evidence for the spread of immune-escape HIV-1 subtype B in the Korean population.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 606 AA, 67781 MW; 218C77457D4DFA8A CRC64;
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Pred. No. 1e-12;
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0015021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000328; ENV GP41.
InterPro; IPR000328; ENV GP41.
InterPro; IPR000777; GP120.
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                                                        Last sequence update)
Last annotation update)
                                                                                                                                Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
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                                                                                                                                                                                                                                                                                                                                                                       AIDS Res. Hum. Retroviruses 16:1047-1053(2000).
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
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PRELIMINARY;
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patient with HIV dementia: evidence for monocyte trafficking into
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SEQUENCE 684 AA; 77266 MW; P9E6F3CCE4D32E10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coat protein; Glycoprotein; Polyprotein; Transmembrane. VCE 729 AA; 81920 MW; 97DA9C4263270381 CRC64;
                                                                                                                                                            Score 138; DB 15; Length 684;
Pred. No. 1.2e-12;
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STRAIN=KRAB12;
Daniels R.S., Patel D., Xiang Z., Zheng N.N., Kang C.;
"Evidence for the spread of immune-escape HIV-1 subtype B
Korean population.";
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                           EMBL; AF217161; AAF75503.1; -. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0019021; C:integral to membrane; IEA. GO; GO:0019031; C:viral capsid; IEA. GO; GO:005198; F:structural molecule activity; IEA. InterPro; IPR000328; Env GP41.
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Matches 25; Conservative
                     J. Neurovirol. 0:0-0(2000)
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Best Local Similarity 96.2%
Matches 25, Conservative
                                                                                                    Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
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Pfam; PF00517; GP41; 1.
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WEDLINE-91374618; PubMed=1895406;
A Daniels R.S., Smith M.H., Fisher A.G.;
Daniels R.S., Smith M.H., Fisher A.G.;
"Molecular characterization of biologically diverse envelope variants of human immunodeficiency virus type 1 derived from an individual.";
J. Virol. 65:5574-5578 (1991).
REMBL, M77575, ABB04111.1;
DR EGO, 60:0019031; C:viral envelope; IEA.
OR GO: 00:0019031; C:viral envelope; IEA.
DR InterPro; IPR000177; GP120.
DR InterPro; IPR000177; GP120.
DR Ffam; PP00516; GP120; 1.
DR Ffam; PF00516; GP120; 1.
DR Ffam; PF00517; GP41; 1.
                                                                                                                                                                                      Daniels R.S., Baddows S., Wilson P., Douglas N.W., Patel D.,
I ves K.J., Easterbrook P., Weber J.N.;
I van association between amino acid substitutions in the 'Silent Face'
I antibody mediated meutralization.";
I Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
I EMBL; AJZ71111; CAB86164.1;
I RMSL; AJZ71111; CAB86164.1;
I ROO; GO:0019028; C:viral capsid; IEA.
I GO; GO:0019028; C:viral capsid; IEA.
I GO; GO:0019031; C:viral envelope; IEA.
I INTERPRO; IPR000777; GPI20.
I INTERPRO; IPR000777; GPI20.
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MEDLINE-88302422; PubMed=2841608;
Risher A.G., Ensoli B., Looney D., Rose A., Gallo R.C., Saag M.S.,
Shaw G.M., Hahn B.H., Wong-Staal F.;
"Biologically diverse molecular variants within a single HIV-1
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676;
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24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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SEQUENCE FROM N.A. MEDLINE=88302422;
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Daniels R.S., Smith M.H., Fisher A.G.;
Daniels R.S., Smith M.H., Fisher A.G.;
Daniels R.S., Smith M.H., Fisher A.G.;
Molecular characterization of biologically diverse envelope variants of human immunodeficiency virus type 1 derived from an individual.";
J. Virol. 65:5574-5578(1991).
BMBL, M13776; AAB04112.1; -.
GO, GO:001931; C:viral envelope; IEA.
GO, GO:001931; C:viral envelope; IEA.
InterPro; IPR000128; Entructural molecule activity; IEA.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP120; 1.
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MEDLINE=88302422: PubMed=2841608;
Fisher A.G., Ensoli B., Looney D., Rose A., Gallo R.C., Saag M.S.,
Shaw G.M., Hahn B.H., Wong-Staal F.;
"Biologically diverse molecular variants within a single HIV-1
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Fisher A.G., Ensoli B., Looney D., Rose A., Gallo R.C., Saag M.S.,
Shaw G.M., Hahn B.H., Wong-Staal F.;
"Biologically diverse molecular variants within a single HIV-1
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein 120/41 (Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein 120/41 (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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RP SEQUEN
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WEDLINE=91374618; PubMed=1895406;

A Daniels R.S., Smith M.H., Fisher A.G.;

A Daniels R.S., Smith M.H., Fisher A.G.;

RT "Molecular characterization of biologically diverse envelope variants

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RT "Virol. 65:5574-5578 (1591).

BT "Of human immunodeficiency virus type 1 derived from an individual.";

RT "Virol. 65:5574-5578 (1591).

BT GO: 00:019028; C:viral capsid; IEA.

BR GO: 00:019028; C:viral capsid; IEA.

BR GO: 00:019031; C:viral envelope; IEA.

BR GO: 00:0019031; C:viral envelope; IEA.

BR GO: 00:0019031; C:viral envelope; IEA.

BR GO: 00:0019031; C:viral molecule activity; IEA.

BR InterPro; IPR000777; 19R20077.
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MEDLINE=91374618; PubMed=1895406;
Daniels R.S., Smith M.H., Fisher A.G.;
Molecular characterization of biologically diverse envelope variants of human immunodeficiency virus type 1 derived from an individual.";
J. Virol. 65:5574-5578(1991).

EMML, M37574; AAB04110.1; -.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP42.
Pfam; PF00516; GP220; 1.
Pfam; PF00517; GP41; 1.
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein 120/41 (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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1es 25; Conservative
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Gaps

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Connor R.I. Korber B.T.M. German B.S., Hahn B.H., Ho D.D.,
Malker B.D., Neumann A.U., Vermund S.H., Mestecky J., Jackson S.,
Walker B.D., Neumann A.U., Vermund S.H., Mestecky J., Jackson S.,
Ra Fenamore E., Cao Y., Gao F., Kalams S., Kunstnan K.J., McDonald D.,
R. McMilliams N., Trkola A., Moore J.P., Wollinsky S.M.; fenamorels.

McMilliams N., Trkola A., Moore J.P., Wollinsky S.M.; fercted by human in munodeficiency virus type 1 while participating in trials of immunodeficiency virus type 1 while participating in trials of immunodeficiency virus type 1 while participating in trials of immunodeficiency virus type 1 while participating in trials of immunodeficiency virus type 1 while participating in trials of immunodeficiency virus type 1 while participating in trials of information of the combinant papers in the combinant papers of integral to membrane; IEA.

M. Virol. 72:1552-1576(1998).

R. EMBL; U84794; AACS8818.1; -
R. GO; GO:0019021; C:viral capsid; IEA.

R. GO; GO:0019021; C:viral envelope; IEA.

R. GO; GO:0005215; Firtansporter activity; IEA.

R. InterPro; IPR000328; ENV GP41.

R. InterPro; IPR005329; Sug_transporter.

R. Ffam; PF00516; GP120; 1.

R. Ffam; PF00517; GP41; 1.
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AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
NON TER
Length 807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 813;
                                                                                                                   99.3%; Score 138; DB 15; Length 8 96.2%; Pred. No. 1.4e-12; ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    041530;
1-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last sequence update)
Last annotation update)
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
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Pred. No. 1.4e-12;
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                                                                                                                                                                                                                                          586 RVLAVERYLKDQQLLGIWGCSGKLIC 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Envelope glycoprotein (Fragment).
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MEDLINE=98105804; PubMed=9445059;
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01-MAY-2000 (TrEMBLrel. 13, C:
01-MAY-2000 (TrEMBLrel. 13, Ls
01-JUN-2003 (TrEMBLrel. 24, Ls
Envelope glycoprotein.
                                                                                                                 Query Match
Best Local Similarity 96.2<sup>3</sup>
Matches 25; Conservative
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les 25; Conservative
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A MEDLINE=94103665; PubMed=8277197;
A MESCOLA J.J., Louwagie J.J., McCutchan F.E., Fischer C.L.,
A Hegerich P.A., Wagner K.F., Fowler A.K., McNeil J.G., Burke D.S.;
A Hegerich P.A., Wagner K.F., Fowler A.K., McNeil J.G., Burke D.S.;
T Two antigenically distinct subtypes of human immunodeficiency virus
T Type 1: viral genotype predicts neutralization serotype.";
J. Infect. Dis. 169:48-54(193).
R MCO GOO1001001; C.integral to membrane; IEA.
R GO; GO:0010028; C.viral capsid; IEA.
R GO; GO:0019031; C.viral envelope; IEA.
R GO; GO:0019031; PST Control molecule activity; IEA.
R InterPro: IPR000328; EDV GP41.
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                                                                                                                           01-JUN-2003 (TrEMBLrel. 13, Last sequence update)
Envelope (Gp160) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        076121;
0.100v-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annocation update)
                                                                                                                                                                                                                                                   Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                                                                      Created)
                                                                          PRT;
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MEDLINE=99294894; Pubmed=10364493;
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Matches 25; Conservative
                                                                          PRELIMINARY;
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Pfam; PF00517; GP41; 1.
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NON TER
SEQUENCE
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                            RESULT 343
Q9QP04
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STRAIN=V1850;
MEDLINE=20192166; PubMed=10725202;
Laukkanen T., Carr J.K., Janssens W., Liitsola K., Gotte D.,
McCutchan F.E., Op de Coul E., Cornelissen M., Heyndrickx L.,
van der Groen G., Salminen M.O.;
"Virtually full-length subtype F and F/D recombinant HIV-1 from Africa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The state of HIV-1 in Thailand.";

Mario Reserve Trues 8:1887-1895 (1992).

Mario Reserve Hum. Retroviruses 1887-1895 (1992).

Mario Reserve Hum. Retroviruses 1887-189.

Mario Retroviruses 188.

Mario Retroviruses 1887-189.

Mario Retroviruses 1887-189.

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MEDLINE=93143998; PubMed=1489577;
McCucchan F.E., Hegerich P.A., Brennan T.P., Phanuphak P.,
Singharaj P., Jugsudee A., Berman P.W., Gray A.M., Fowler A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Albert J.K., Kim B., Sanders-Buell E., Salminen M.O., Alaeus A., Albert J.A., Birx D.L., McUtchan F.E.;
"HIV-1 isolate VI850 from Zaire, complete genome.";
Submitted (JUL.1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF077336; AAD46094.1;
GO; GO:0010021; C:integral to membrane; IEA.
GO; GO:0019021; C:integral to membrane; IEA.
GO; GO:0019028; C:irial capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:001981; F:structural molecule activity; IEA.
InterPro; IPR000777; GP120.
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NCE 832 AA; 93809 MW; 4CE00FD6D9DE269B CRC64;
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Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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Viruses; Retrold viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                                                                                and South America.";
Virology 269:95-104(2000)
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Best Local Similarity 96.2%
Matches 25; Conservative
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Pfam; PF00517; GP41; 1.
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                                                                                                                       SEQUENCE FROM N.A.
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                                                                 NCBI TaxID=11676;
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"HIV Type I variants Transmitted to Women in Kenya Require the CCR5
"Toreceptor for Entry, Regardless of the Genetic Complexity of the
Infecting Virus ";
AIDS Res. Hum. Retroviruses 18:567-576(2002).

REBL, AF401148; AAM66195.1;
GO; GO:0016021; C:interapt to membrane; IEA.

GO; GO:0015028; C:viral capsid; IEA.

GO; GO:0019031; C:viral capsid; IEA.

RO; GO:0019031; C:viral molecule activity; IEA.

RICHEPRO; IPR00077; GP120.

RICHEPRO; IPR00077; GP120.

REPRO; GO:0015028; Env GP41.

RICHEPRO; IPR0017; GP120.

REPRO; GO:0015028; Env GP41.

REPRO; GO:0015028; Env GP41.

REPRO; GR120; I.

REPRO; GR120; I.
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MEDILTRE=2203141; PubMed=12036486;
MEDILTRE=2203141; PubMed=12036486;
LONG E.M., Rainwater S.M., Lavreys L., Mandaliya K., Overbaugh J.;
"HIV Type 1 Variants Transmitted to Women in Kenya Require the CCRS
Correceptor for Entry, Regardless of the Genetic Complexity of the
Infecting Virus "; The Type 1 B1567-576 (2002).
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                                  Length 835;
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Pred. No. 1.4e-12;
1; Mismatches 0; Indels 0
                                                                  Indels
94918 MW; 46E3566D8B0C92D6 CRC64;
                                                                                                                                                                                                                                               (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                 Score 138; DB 15;
Pred. No. 1.4e-12;
                                                                                                                                                                                                                   837 AA
                           Query Match
99.3%; Score 138; DB
Best Local Similarity 96.2%; Pred. No. 1.4e
Matches 25; Conservative 1; Mismatches
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1es 25; Conservative
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835 AA;
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SEQUENCE FROM N.A.
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01-OCT-2002 (
01-OCT-2003 (
SEQUENCE
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08JDN0
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                                                             InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 837 AA; 94748 MW; 60B366124081226F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 838 AA; 95247 MW; 127128F8F5DIF86B CRC64;
                                                                                                                                                                              Query Match
99.3%; Score 138; DB 15; Length 837;
Best Local Similarity 96.2%; Pred. No. 1.4e-12;
Matches 25; Conservative 1; Mismatches 0; Indels (
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF193277, AMF22331.;
GO, GO:0019028; C:integral to membrane; IEA.
GO, GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; P:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0013028; C:viral capsid; IEA.
GO; GO:0013031; C:viral envelope; IEA.
GO; GO:0005198; E:structural molecule activity; IEA.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
Nob_TaxID=11676;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein.
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Job time : 127 secs
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MEDLINE=20386750; PubMed=10933619;
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Matches 25, Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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139
1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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DT 01-OCT-1989 (Rel. 12, Created)
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LY to induce syncytium-independent
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P19551;
01-FRB-1991 (Rel. 17, Created)
01-FRB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP41)].
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11704;
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Pred. No. 1.4e-13;
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MEDLINE=90317877; PubMed=1695254;
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Best Local Similarity 100.0%;
Matches 26; Conservative 0
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PDB; LAIK; 16-UUN-97
ILIK: 16-UUN-97
INTERPRO, IPRO000328; Env GP41.
InterPro; IPR000177; GP120.
Pfam; PF00516; GP41; 1.
Pfam; PF00517; GP41: 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
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01-OCT-1989 (Rel. 12, Last sequence update)
Le-OCT-2001 (Rel. 40, Last annotation update)
Envelope polyprotein Gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
                                                                  Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11683;
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PIR; S54384; S54384.
HIV; M22639; ENV$2226.
InterPro; IPR000728; Env GP41.
InterPro; IPR00777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
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TRANSMEMBRANE GLYCOPROTEIN.
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Submitted (NOV-1988) to the HIV data bank
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Gene 52:71-82(1987).
                                                                           Gaps
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13-AUG-1987 (Rel. 05, Last sequence update)
15-AUL-1999 (Rel. 38, Last ennotation update)
15-UUL-1999 (Rel. 38, Last ennotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11708;
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InterProj IPR000328; Env. GP41.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
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MEDLINE-87248097; PubMed=3036660;
Srinivasan A., Anand R., York D., Ranganathan P., Feorino P., Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
   Length 853;
                                                                           Indels
Score 139; DB 1;
Pred. No. 1.4e-13;
Query Match
100.0%; Score 139; I
Best Local Similarity 100.0%; Pred. No. 1.4
Matches 26; Conservative 0; Mismatches
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PIR; D26192; VCLJZR.
HIV; K03458; ENV$Z6.
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P04578; 009779;
13-AUG-1999 (Rel. 05, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane]
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AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
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Pred. No. 1.4e-13;
                                       EXTERIOR MEMBRANE GLYCOPROTEIN. TRANSMEMBRANE GLYCOPROTEIN.
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AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
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                                                                                                   MEDLINE=87299196; PubMed=1040055;
Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
Gallo R.C., Wong-Staal F.;
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                                                                                                                                             'Complete nucleotide sequences of functional clones of the AIDS
                                                                                                                                                                                                             Rather L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.,
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
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BY SIMILARITY.

N-LINKED (GLCNAC. ...) (POTENTIAL N-LINKED) (GLCN
                                   Human immunodeficiency virus type 1 (HXB2 isolate). (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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EMBL; AF033839; AAB9976.1; --
EMBL; AF033819; AAC82596.1; --
EMB; LDF4; Z6-JAN-00.
PDB; LDF5; Z6-JAN-00.
PDB; LDF5; Z6-JAN-00.
PDB; LGC1; 19-AUG-98.
PDB; LGC1; 19-AUG-98.
PDB; LGC1; 10-CCT-02.
PDB; LX34; L0-CCT-01.
PDB; LX34; L0-CCT-01.
PDB; LX34; L0-CCT-01.
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InterPro, IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
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                                                            NCBI_TaxID=11706;
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MEDLINE=95127297; PubMed=7826699;
MEDLINE=95127297; PubMed=7826699;
Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HTLV type 1 IIIB).";
AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
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PDB; 11R3; 02-MAY-01.
GlycoSuiteDB; Q70626; -
InterPro; 1PR000328; Env. GP41.
InterPro; IPR00077; GP120.
Pffam; PF00516; GP120, 1.
Pffam; PF00516; GP120, 1.
ALDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
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Q70526;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 32, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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(See http://www.isb-sib.ch/announce/
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                                     EMBL, K02083; AAB59873.1; -.
EMBL, X01762; CAA25903.1; ALT_SEQ.
PIR; A03974; VCLJVL.
INTEPPRO, IPR000328; Env GP41.
InterPro; IPR00077; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP413; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
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MEDLINE=85111157; PubMed=2982104;
Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP1)].
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"Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovirus.";
Nature 313:450-458(1985).
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Pred. No. 1.4e-13;
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10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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                               Human immunodeficiency virus type 1 (BRU isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                             SEQUENCE FROM N.A.
MEDLINE=85099333; PubMed=2981635;
Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
"Nucleotide sequence of the AIDS virus, LAV.";
Cell 40:9-17(1985).
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R HIV; M21138; ENV$JH3.
R InterPro; IPR000328; Env GP41.
R InterPro; IPR000328; Env GP41.
R Pfam; PR00516; GP120; 1.
R Pfam; PR00517; GP41; 1.
R Pfam; PR00517; GP41; 1.
SIGNAL 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
T CHAIN 517 867 TRANSMEMBRANE GLYCOPROTEIN.
T DISULPID 53 73 BY SIMILARITY.
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01-OCT-1989 (Rel. 12, Last sequence update)
15-UUL-1999 (Rel. 18, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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TRANSMEMBRANE GLYCOPROTEIN.
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL)
                                                                                                                                                                                  100.0%; Score 139; DB 1; Length 861; 100.0%; Pred. No. 1.4e-13;
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MEDLINE=89352108; PubMed=2669897;
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us-09-733-239-1.rsp

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ENV_HV1BN
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Pfam; PF00517; G40120; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal; 3D-structure.
31 1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.
CHAIN 503 847 TRANSMEMPRANE GLYCODPOTEIN.
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Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
"Viral determinants of human immunodeficiency virus type 1 T-cell or
macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
J. Virol. 64:4390-4398(1990).
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01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
                                                              (POTENTIAL).
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Pred. No. 1.5e-13;
Mismatches 0; Indels (
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TRANSMEMBRANE GLYCOPROTEIN.
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
COLE_TaxID=11691;
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InterPro; IPR000777; GP120.
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ilarity 100.0%;
Conservative 0;
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Best Local Simil
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-!- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS
-HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
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01-0CT-1989 (Rel. 12, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein Gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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Pred. No. 2e-13;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11693;
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MEDLINE=89085613; PubMed=2789516;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch)
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STANDARD; PRT; 855 AA

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DT 01-FEB-1991 (Rel. 17, Created)

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PIR; A31667; VCLUBR.
PDS; IIM7, 23-OCT-02.
HIV; M21099; ENV$BRVA.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00517; GP120; 1.
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Matches 25; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
                                                                                                                                                                                           Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S "A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot.";
AlDS 3:707-715[1989]
-1- MISCELLANEOUS: THE OYI ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONESE INDIVIDUAL.
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HIV; M26727; ENV$OXI.
INTERPO: IPR000328; ENV GP41.
INTERPPO: IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Transmembrane;
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                                                                          Human immunodeficiency virus type 1 (OYI isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11699;
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MEDLINE=90148544; PubMed=2559749;
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SEQUENCE FROM N.A.
MEDLINE=89228766; PubMed=2713163;
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HIV; M15896; ENV$Z321.
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Matches 25; Conservative
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InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                      13-AUG-1987 (Rel. 05, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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                         Score 138; DB 1; Length 855;
Pred. No. 2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11707;
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                                                Local Similarity 96.2
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PDB; 1JAV; 17-OCT-01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-UUL-1999 (Rel. 138, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1 (Zaire HZ321 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11692;
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InterPro; IPR00077; GP120.
Pfam; PP00516; GP120; 1.
Pfam; PP00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                score 137; DB 1; Lens
No. 2.9e-13;
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1; Mismatches
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EMBL, M18429; AAB03749.1; -.
PDB; 1CE4; 18-MAR-99.1; -.
HIV; M38429; ENV$JRCSF.
HIV; M38429; ENV$JRCSF.
InterPro; IPR00328; Env GP41.
InterPro; IPR00316; GP120, 1.
Pfam; PF00517; GP41; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal; 3D-structure.
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01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
12-OCT-2003 (Rel. 42, Last annotation update)
13-Yeloge polyprotein (GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].
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TRANSMEMBRANE GLYCOPROTEIN.
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
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Pred. No. 4.1e-13;
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ENV HV1JR
D ENV HV1JR
AC P20871;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane DE GIVCOprotein (GP120); Transmembrane glycoprotein (GP120);
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11688;
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KOyanagi S., Chen I.S.Y.;
Submitted (DEC-1988) to the HIV data bank.
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InterPro; IPR000328; Env GP41.
InterPro; IPR000328; Env GP41.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal; SIGNAL 1.
                                                                                                            "Complete nucleotide sequence, genome organization, and biological properties of human immunodeficiency virus type 1 in vivo: evidence for limited defectiveness and complementation.";
J. Virol. 66:6587-6600(1992).
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MEDILINE=93021387; PubMed=1404605;
Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
Shaw G.M.;
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PIR; H44001; H44001.
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Length 843;

Score 135; DB 1; Pred. No. 5.9e-13;

97.1%; 92.3%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE 86235450; PubMed=3012778;
Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
"Genetic variation in HTLV-III/LAV over time in patients with AIDS or
at risk for AIDS.";
Science 232:1548-1535(1986).
-!- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
BLOOD SAMPLES SEQUENTIALLY TAKEN FROM
BLOOD SAMPLES SEQUENTIALLY TAKEN FROM
WAS PERINATALLY INFECTED BY HER MOTHER.
Gaps
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01-NOV-1988 (Rel. 09, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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SIGNAL 1 29
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InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
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24; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] — SEQUENCE FROM N.A. MEDLINE-85090453; PubMed=2578227; Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S., Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A., Levy J.A., Dina D., Luciw P.A., "Nucleotide sequence and expression of an AIDS-associated retrovirus
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11685;
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92.3%;
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AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
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MEDLINE=90117906; PubMed=2370688;
YORK-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
"Human immunodeficiency virus type 1 cellular host range,
replication, and cytopathicity are linked to the envelope region of
the viral genome.";
J. Virol. 64:4016-4020(1990).
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ID ENV 47153

AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 10-FEB-1991 (Rel. 17, Last sequence update)
DT 10-FCB-2901 (Rel. 142, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane Envelope polyprotein (GP120); Transmembrane glycoprotein (GP41)].
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VGB__TaxID=11690;
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EXTREIGN MEMBRANE GLYCOPROTE:
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HIV; M38427; ENVSSF33.
InterPro; IPR000328; ENV_GP41.
InterPro; IPR000777; GP1Z0.
Pfam; PP00516; GP120; 1
Pfam; PP00517; GP417; 1.
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                                                                                                                             MEDLINE=88219542; PubMed=3369091;
MEDLINE=88219542; PubMed=3369091;
Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
"Envelope sequences of two new United States HIV-1 isolates.";
Virology 164:531-536(1988).
-! MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
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TRANSMEMBRANE GLYCOPROTEIN.

BY SIMILARITY.

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INTERPROPOSTORS; ENV GP41.
INTERPRO, IPRO00777; GP120.
Pfam; PF00517; GP41; 1.
Pfam; PF00517; GP41; 1.
Signal.
I 29 EXTERIOR MEMBRANE GLYCOPROTEIN.
CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
                   Human immunodeficiency virus type 1 (SC isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
      glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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HIV; M17450; ENV$SC.
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01-NOV-1988 (Rel. 09, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane
                                                      | PIR; A03976; VCLJA2. | CLJA2. | CLJA2
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
17-JUL-1999 (Rel. 38, Last annotation update)
18-JUL-1999 (Rel. 38, Last annotation u
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MEDLINE=86218077; PubMed=2423250;
Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wol Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
"Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS.";
                   (POTENTIAL)
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Signal.
1 29 EXTERIOR MEMBRANE GLYCOPROTEIN. CHAIN 520 865 TRANSMEMBRANE GLYCOPROTEIN. DISULFID 53 73 BY SIMILARITY. DISULPID 118 218 BY SIMILARITY.
DISULPID 118 BY SIMILARITY.
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NCBI_TaxID=11701;
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N-LINKED (GLCNAC...) (POTI
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HIV; M17451; ENV$RF.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PP00516; GP120; 1.
Pfam; PF00517; GP121.
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      Cell 45:637-648(1986).
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-!- MISCELLANDOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
WAS PERINATALLY INPECTED BY HER MOTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-86218077, PubMed=2423250;

Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf

Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;

Tdentification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS.";
                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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BY SIMILARITY.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCDI_TaxID=31678;
                                                                                                      97.1%; Score 135; DB 1; Length 856; 92.3%; Pred. No. 6e-13;
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                                                                                                                                                                                                                                                                                                                                     856 AA.
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PDB; 1LB0; 04-DEC-02.
PDB; 1LCX; 04-DEC-02.
InterPro; 1PR000328; Env GP41.
InterPro; 1PR00077; GP120.
Pfam; PF00516; GP120; 1.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
    "Characterization of the secreted, native gp120 and gp160 of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYCOPROTEIN (GP120)
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PIR; C25523; VCLJH4.
HIV; M13137; ENV$CD645.
InterPro; IPR000328; Env GP41.
InterPro; IPR00077; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
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Pred. No. 6.1e-13;
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AIDS Res. Hum. Retroviruses 6:371-380(1990).
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MEDLINE=90253924; PubMed=2187500;
Kalyanaraman V.S., Rodriguez V., Veronese F., Rahman R., Lusso P.,
DeVico A.L., Copeland T., Oroszlan S., Gallo R.C., Sarngadharan M.G.;
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01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11687;
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R PDB; 1RS2; 29-DEC-99.
R PDB; 1NCY; 31-JUL-94.
R PDB; 1NIZ; 25-FEB-03.
R PDB; 1NNO; 25-FEB-03.
R InterPro; 1PR000777; GP120.
R InterPro; 1PR000777; GP120.
R InterPro; 1PR000777; GP120.
R Pfam; PF00517; GP41; 1.
R AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal; JD-structure.
R AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal; JD-structure.
R SIGNAL
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DISULFID 130 513 EXTERIOR MEMBRANE GLYCOPROTEIN.
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T DISULFID 301 335 BY SIMILARITY.
T DISULFID 301 335 BY SIMILARITY.
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MEDLINE=88219542; PubMed=3369091;
Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.,
"Envelope sequences of two new United States HIV-1 isolates.";
Virology 164:531-536(1988).
-!- MISCELLANBOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
                                                                             01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
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ENV_HV1MN
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MEDLINE=86245056; PubMed=2424612;
Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
"Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients.";
Cell 46:63-74(1986).
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13-540G-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40). Inst annotation update)
16-OCT-2001 (Rel. 40). Inst annotation update)
19-Voorotein (GP120); Transmembrane glycoprotein (GP11)].
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Pfam; PF0516; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
Signal. 1 31 BY SIMILARITY.
CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
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EMBL; A07108; CAA00616.1; -.
HIV; K03454; ENV$ELI.
INCEPPC; IPR000328; ENV GP41.
INTERPC; IPR000777; GP120.
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MEDLINE-92351552; PubMed=1322587;
Shimizu H., Hasebe F., Tsuchie H., Morikawa S., Ushijima H.,
Kitamura T.;
"Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated transmembrane glycoprotein.";
Virology 189:534-546(1992)
-!- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR UAG OCCURS BETWEEN
THE CODONS FOR 729-ALA AND 730-ARG.
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01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP12).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
Viruses138375;
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                                                                 EMBL; D12562; BAA02124.1; ALT_SEQ.
PIR; A42995; VCLJKB.
InterPro; IPR000328; Env GP41.
InterPro; IPR000516; GP120; 1.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
Alms; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
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EXTERIOR MEMBRANE GLYCOPROTEIN.
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larity 88.5%; Pred. No. 1.8e-12;
Conservative 2; Mismatches 1;
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ID ENV HV1ND

AC P18799;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
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98116 MW;
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1 RILAVERYLKDOOLLGIWGCSGKLIC 26
                   Best Local Similarity 84.6
Matches 22; Conservative
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ENV HV128
ID ENV HV128
AC P05882;
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                                                                                                                                                                                                          human immunodeficiency virus.";
Gene 81:275-284(1989).
-!- MISCELLANBOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH
AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.
                                                                                                                                                         Spire B., Sire J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F., Hampe A., Chermann J.C.; "Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the
                     membrane
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                                                              Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11695;
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior m
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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                                                                                                        Gaps
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MEDLINE=88281278; PubMed=3395517;
Yourno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
Gallo R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-UUL-1999 (Rel. 138, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIDS Res. Hum. Retroviruses 4:165-173(1988).
-!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
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HIV; J03653; ENV$JY1.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
89.9%; Score 125; DB 1; Length 846; 84.6%; Pred. No. 2.1e-11; ive 3; Mismatches 1; Indels
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11681;
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us-09-733-239-1.rsp

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MEDLINE=86245056; PubMed=2424612;
Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
"Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients.";
Cell 46:63-74(1986).
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ENV HV1MA

AC P04583;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-19987 (Rel. 05, Last sequence update)
DT 15-ULD-1999 (Rel. 38, Last annotation update)
DE Envelope polyprotein (GP120); Transmembrane glycoprotein (GP20); Transmembrane glycoprotein (GP20); Transmembrane glycoprotein (GP41)].
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
VirusesTaxID=11697;
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EMBL; A07116; CAA00623.1; -.
PIR; T01672; T01672.
HIV; K03456; ENV$MAL.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
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MEDLINE=902559077; PubMed=2188136;
Huct T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
Huct Grganization of a chimpanzee lentivirus related to HIV-1.";
Nature 345:356-359(1990).
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01-AUG-1990 (Rel. 15, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein 09160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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InterProj IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
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88.5%; Pred. No. 2.2e-11;
iive 1; Mismatches 2; Indels
                                                                                      | N. LINKED (GLCNAC. . . ) (POTINED (GLCNAC. . ) (POTINE
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HIV, X52154, ENV$CPZ.
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les 23; Conservative
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King N.W., Daniel M.D., Desrosiers R.C.; "Comparison of simian immunodeficiency virus isolates."; Nature 311:619-622 [1988].
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Matches 13; Conservative
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MEDLINE=88122665; PubMed=2893293;
Kestler H.W., Li Y., Naidu Y.M., Butler C.V., Ochs M.F., Jaenel G.,
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Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
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01-NOV-1988 (Rel. 09, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior glycoprotein (GP120); Transmembrane glycoprotein (GP41)]
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80.8%;
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Best Local Similarity 80...
Best Local 21; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=92260681; PubMed=1583738;
Mulligan M.J., Yamshchikov G.V., Ritter G.D. Jr., Gao F., Jin M.J.,
Mail C.D., Spies C.P., Hahn B.H., Compans R.W.;
"Cytoplasmic domain truncation enhances fusion activity by the
exterior gyroproteain complex of human immunodeficiency virus type 1
in selected cell types."
J. virol. 66:3971-3975(1992).
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P32536;
01-OCT-1993 (Rel. 27, Lorated)
01-OCT-1999 (Rel. 27, Lost sequence update)
15-JUL-1999 (Rel. 38, Lost annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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IN-FRAME TERMINATION CODON.

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).
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Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane.
NON TER 1 1 RYPERION MEMBRANE.
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Pred. No. 2.1e-05;
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HIV; X06879; BNV$MAZ51.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
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Nucleic Acids Res. 18:6142-6142(1990)
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MEDLINE=91045094; PubMed=2235509;
MEDLINE=91045094; PubMed=2235509;
Kuehnel H., Kreutz R., Ruebsamen-Waigmann H.;
"Nucleotide sequence of HIV-2D194, an isolate from a Gambian case of "Nucleotide sequence of HIV-2D194, an isolate from a gambian case of 'neuro-AIDS', which showed excellent growth in macrophages.";
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01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprocein (9160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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            EMBL; M86924; AAA43938.1; -.
PIR; A42555; VCLJS4.
InterPro; IPR000328; Env GP41.
InterPro; GPT00777; GPI20.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS.
A.Coat protein; Polyprotein; Glycoprotein; Transmembrane;
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EXTERIOR MEMBRANE GLYCOPROTEIN.
TRANSMEMBRANE GLYCOPROTEIN.
POTENTIAL.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11713;
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Pred. No. 5.9e-05;
6; Mismatches 7; Indels
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SEQUENCE OF 1-266 FROM N.A.

SEQUENCE OF 1-266 FROM N.A.

Ruchnel H., von Briesen H., Dietrich U., Adamski M., Mix D.,

Biesert L., Kreutz R., Immelmann A., Henco K., Meichener C.,

Andreesen R., Gelderblom H., Ruchbamann-Waigmann H.,

Molecular cloning of two west African human immunodeficiency virus

type 2 isolates that replicate well in macrophages: a Gambian

isolate, from a patient with neurologic acquired immunodeficiency
syndrome, and a highly divergent Ghanian isolate immunodeficiency

Proc. Natl. Acad. Sci. U.S. A. 86:2383-2387(1989).

- MISCELLANEOUS: THIS ISOLATE IS FROM A GAMBIAN CASE OF
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50.0%; Pred. No. 7.1e-05;
ilve 6; Mismatches 7;
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EMBL; X5223; CAA36471.1; -.
EMBL; X512159; S12159.
HIV; J04542; ENV$2D194.
InterPro; IPR000328; ENV GP41.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP120; 1.
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les 13; Conservative
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                                                                                                                                       MEDLINE=90122350; PubMed=2611042;
MEDLINE=90122350; PubMed=2611042;
Hasegawa A., Tsujimoto H., Maki N., Ishikawa K.I., Miura T.,
Pukasawa M., Miki K., Hayami M.;
"Genomic divergence of HIV-2 from Ghana.";
AIDS Res. Hum. Retroviruses 5:593-604(1989).
-!- MISCELIANEOUS: READTHROUGH OF TERMINATOR UAG BETWEEN CODONS UUG
FOR 738-LEU AND CCU FOR 739-PRO MAY OCCUR.
                                          01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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                                                                                      Human immunodeficiency virus type 2 (isolate Ghana-1) (HIV-2). Viruses; Retroid viruses; Retroviridae; Lentivirus.
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851 AA;
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ENV_HV2G1
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AC_P18040;
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MEDLINE=88320359; PubMed=3261862;
Zagury J.F., Franchini G., Reitz M.S. Jr., Collalti E., Starcich B.R., Hall L., Fargnoli K., Jagodzinski L.L., Guo H.-G., Laure F., Arya S.K., Josephs S.F., Zagury D., Wong-Staal F., Gallo R.C., "Genetic variability between isolates of human immunodeficiency virus (HIV) type 2 is comparable to the variability among HIV type 1."; Proc. Natl. Acad. Sci. U.S.A. 85:5941-5945(1988).
                              Gaps
                                                                                                                                                                                   01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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HIV; J03654; ENV$2NIHZ.
InterPro; IPR000328; Env GP41.
InterPro; IPR000516; GP120.
Pfam; PP00516; GP120; 1.
Pfam; PP00577; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
                                                                                                                                                                                                                                                              Human immunodeficiency virus type 2 (isolate NIH-Z) (HIV-2)
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11719;
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Length 851,
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N-LINKED (GLCNAC. . .) (POTE
 59.7%; Score 83; DB 1; 150.0%; Pred. No. 7.1e-05;
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Matches 13; Conservative
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Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
             366
398
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                                                                                                                                                                                                   Gaps
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ENV HV2CA

AC P24105;
DT 01-MAR-1992 (Rel. 21, Created)
DT 11-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DF 15-JUL-1999 (Rel. 38, Last annotation update)
DF Shvelope polyprotein (GP100); Transmembrane glycoprotein (GP41)].
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TRANSMEMBRANE GLYCOPROTEIN.
N-LINKED (GLCNAC. .) (POTENTIAL.
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PIR; F38475; VCLJCT.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=91170959; PubMed=2005437;
Tristem M., Hill F., Karpas A.;
"Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus type 2 proviral clone (HIV-2CAM2).";
J. Gen. Virol. 72:721-724(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 2 (isolate CAM2) (HIV-2). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                        Length 856;
                                                                                                                           Score 83; DB 1; Lengtu conved. No. 7.2e-05;
                                                                                                             A938B0A7E2B881D6 CRC64;
  (GLCNAC. ..)
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RVTAIEKYLKDQAQLNSWGCAFRQVC 594
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Local Similarity 50.0%;
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TRANSMEMBRANE GLYCOPROTEIN
(BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL N-LINKED (GLCNAC. . .)
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NCB1_TaxID=11716;
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                                                                                                                                                                                                                                                Length 859;
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01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior
                                                                                                                                                                                                                                             Score 83; DB 1; Length 859
Pred. No. 7.2e-05;
6; Mismatches 7; Indels
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                                                                                                                                                                                                     MW; 6F54913F206B26C3 CRC64;
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SEQUENCE OF 1-207 FROM N.A.
SEQUENCE OF 1-207 FROM N.A.
MEDLINE=90081881; PubMed=2594088;
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Nature 342:948-950(1989).
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Ruebsamen-Waigmann H.;
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PIR; S24571; S24571.
HIV; X16109; BNV$2D205.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-87287230; PubMed-3649576;
Chakrabarti L., Guyader M., Alizon M., Daniel M.D., Desrosiers R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENV SIVM1 STANDARD; PRT; 882 AA.
P05885; Q85725; Q85726;
01-NOV-1988 (Rel. 09, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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Pred. No. 7.2e-05;
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6; Mismatches 7; Indels
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Best Local Similarity 50.00.
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MEDILIRE=90112662; PubMed=2296086;
Kumar P., Hui H., Kappes J.C., Haggarty B.S., Hoxie J.A., Arya S.K.,
Shaw G.M., Hahn B.H.;
"Molecular characterization of an attenuated human immunodeficiency
J. virus type 2 isolate.";
J. Virol. 64:890-901(1990).
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01-FBE-1996 (Rel. 33, Last sequence update)
15-ULL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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HIV; M31113; ENV$2ST.
InterPro: IPR0000328; Env GP41.
InterPro: IPR00077; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.

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Pred. No. 7.2e-05;
6; Mismatches 7; Indels
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Best Local Similarity 50.0%;
Matches 13; Conservative 6
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RESULT 39
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AC_P19503;
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MEDLINE=89262053; PubMed=2786147;
MEDLINE=89262053; PubMed=2786147;
MEDLINE=89262053; PubMed=2786147;
Missch V.M., Olmstead R.A., Murphey-Corb M., Purcell R.H.,
Johnson P.R.;
"An African primate lentivirus (SIVsm) closely related to HIV-2.";
Nature 339:389-392(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simian immunodeficiency virus (F236/smH4 isolate) (sooty mangabey) Viruses; Retroid viruses; Retroid viruses; Retroididae; Lentivirus.
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01-0cr-1989 (Rel. 12, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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      EMBL; Y00277; -; NOT_ANNOTATED_CDS.
PIR; H28887; VCLJG3.
HIV; M16403; ENV$MM142.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41: 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
SIGNAL.
1 22
                                                                                          MEMBRANE GLYCOPROTEIN.
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Pred. No. 7.4e-05;
6; Mismatches 7; Indels
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IN-FRAME TREMINATION CODON,
N-LINKED (GLCNAC. ) (POTE)
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Best Local Similarity 50.0%;
Matches 13; Conservative
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MEDLINE-90272009; PubMed=1971917;
Dewhurst S., Embretson J.E., Anderson D.C., Mullins J.I., Fultz P.N.;
"Sequence analysis and acute pathogenicity of molecularly cloned
SIVGNM-PBj14.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simian immunodeficiency virus (PBj14/BCL-3 isolate) (sooty mangabey)
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11738;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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HIV; X14307; ENVSSMMH4.
INCEPPRO; IPR000028; ENV GP41.
INCEPPRO; IPR000777; GP120.
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Best Local Similarity 50.03
Matches 13; Conservative
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Pfam; PF00517; GP41; 1.
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         MEDLINE-90232731; PubMed=2158689;
Baier M., Garber C., Mueller C., Cichutek K., Kurth R.;
"Complete nucleotide sequence of a simian immunodeficiency virus from
                                          African green monkeys: å novel type of intragroup divergence.";
Virology 176:216-221(1990).
-!- MISCELLANEOUS: This is an African green monkey isolate.
                                                                                                                                                                      EMBL; M30931; AAA91919.1; -.
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       Dewhurst S., Embrecson J.E., Fultz P.N., Mullins J.I.; Molecular clones from a non-acutely pathogenic derivative of SIVsmmPBj14: characterization and comparison to acutely pathogenic
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01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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MW; 1438BD23B900D0AA CRC64;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VGBI_TaxID=11730;
                                          clones.";
AIDS Res. Hum. Retroviruses 8:1179-1187(1992).
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HIV; M31325; ENV$SMMPBJ.
InterPro; IPR000328; ENV GP41.
Pitareryo; IPR00077; GP1<u>2</u>0.
Pfam; PP00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Gl
 MEDLINE=92368737; PubMed=1503826;
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01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last annotation update)
19-OCT-2001 (Rel. 40, Last annotation update)
19-OCT-2001 (GP120); Transmembrane glycoprotein (GP41)].
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PIR; C46356; C46356.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00517; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
                                                                                                                  GLYCOPROTEIN.
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Pred. No. 0.00011;
6; Mismatches 7; Indels
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AC Q02837; 99
DT 01-ULL-1993
DT 16-OCT-2001
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                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=88332906; PubMed=3374586;
MEDLINE=88332906; PubMed=374586;
Mixi R., Kitamura T., Hayama A., Morikawa S., Tsujimoto H.,
Mixi K., Kitamura T., Hayami M.,
"Sequence of simian immunodeficiency virus from African green monkey,
a new member of the HIV/SIV group.",
Nature 333:457-461(1988).
-!- MISCELLANEOUS: This is an African green monkey isolate.
        01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
Signal.
SIGNAL 1 20
                                                                          Simian immunodeficiency virus (TYO-1 isolate) (SIV-AGM) Viruses; Retroid viruses; Retroviridae; Lentivirus.
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PIR, G30045; VCLJG4.
HIV; X07805; ENV$AGMTY.
INLETPC9; IPR000328; ENV G941.
InterPro; IPR000777; GP120.
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@isb-sib.ch)
                                                   SEQUENCE FROM N.A.
MEDLINE=91220680; PubMed=2024476;
Pomsgaard A., Hirsch V.M., Allan J.S., Johnson P.R.;
A highly divergent proviral DNA clone of SIV from a distinct species of African green monkey.";
Virology 182:397-402(1991).
I MISCELLANBOUS: This is an African green monkey isolate.
                                                                                                                                                                                                                                                                                                                                       Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
SIGNAL 1 24 POTENTIAL.
Simian immunodeficiency virus (isolate AGM / clone GRI-1) (SIV-AGM)
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=31684;
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EMBL; M58410; AAA47591.1; -.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
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       01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Coat protein GP32; Putative protein ENV-EXTN)
                                                                                                   SEQUENCE FROM N.A.

MEDLINE-81187627; PubMed=3646094;

Hirsch V., Riedel N., Mullins J.I.;

"The genome organization of STLV-3 is similar to that of the AIDS viva except for a truncated transmembrane protein.";

Cell 49:307-319(1987).

-i MISCELLANEOUS: THIS IS A MACAQUE ISOLATE.
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Pred. No. 0.00015;
7; Mismatches 7; Indels
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                                                                     Simian immunodeficiency virus (K78 isolate) (SIV-MAC).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11736;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90156504; PubMed=2304139;
Johnson P.N., Romsgaard A., Allan J., Gravell M., London W.T.,
Ollmstead R.A., Hirsch V.M.;
"Simian immunodeficiency viruses from African green monkeys display
                                                                                                                                                                                 01.AUG-1992 (Rel. 23, Last sequence update)
[6-OCT-2001 (Rel. 40, Last annocation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
                                                                                                                                                                                                                                                                                                                                                                                                                                           unusual genetic diversity.";
J. Virol. 64:1086-1092(1990).
-!- MISCELLANEOUS: THE 155 ISOLATE IS FROM A MONKEY IMPORTED FROM
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InterPro; IPR000328; Env GP41.
InterPro; IPR00077; GP120.
Pfam; PF00517; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Transmembrane;
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TRANSMEMBRANE GLYCOPROTEIN.
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                                                                                                                                                                                                                                                                     Simian immunodeficiency virus (AGM155 isolate) (SIV-AGM) Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TaxID=11727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B50A7F9C9005D8D9 CRC64;
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01-AUG-1992 (Rel. 23, Last seq
16-OCT-2001 (Rel. 40, Last ann
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Best Local Similarity

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   Gaps
                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein 09160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U22047; AAA64582.1; -.

R InterPro; IPR000328; Env GP41.

R Péam; PF00516; GP120.

R Pfam; PF00517; GP41; 1.

A AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.

R CHAIN 20 503 EXTERIOR MEMBRANE GLYCOPROTEIN.

CHAIN 504 857 TRANSMEMBRANE GLYCOPROTEIN.

CHAIN 504 857 TRANSMEMBRANE GLYCOPROTEIN.

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Indels
                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 2 (isolate KR) (HIV-2) Viruses; Retroid viruses; Retroviridae; Lentivirus.
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ID ENV HV2KR
AC Q74126;
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Length 857;

DB 1; L 0.00021;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                       MEDLINE=87287229; PubMed=3497350; Gurgo C., Callatti E., Franchini G., Gall D. R.C., Guv H.-G., Gurgo C., Callatti E., Fargnoli K., Hall L., Wong-Staal F., Reitz M.S. Jr.; "Sequence of simian immunodeficiency virus and its relationship to the human immunodeficiency viruses.";
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HIV; M15897; ENV$K6W78.
INTERPO; IPR00077; GP120.
InterPro; IPR00077; GP120.
Flam; PF00516; GP1120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTERIOR MEMBRANE GLYCOPROTEIN. TRANSMEMBRANE GLYCOPROTEIN. IN-FRAME TERMINATION CODON.
                                                                                                                         01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-JUL-1999 (Rel. 136, Last annotation update)
Envelope polyportein GP160 precursor [Contains: Exterior glycoprotein (GP120); Transmembrane glycoprotein (GP120)].
                                                                                                                                                                                            Simian immunodeficiency virus (K6W isolate) (SIV-MAC). Viruses, Retroid viruses, Retroviridae, Lentivirus.
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-!- MISCELLANEOUS: THIS IS A MACAQUE ISOLATE.
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7; Mismatches
                                            570 RVTAIEKYLRDQARLNSWGCAFRQVC 595
                      1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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                                                                                                  Gaps
761 N-LINKED (GLCNAC. . .) (POTENTIAL)
101184 MW; 9052B543777DD979 CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: GP120; GP32;
Putative protein ENV-EXIN].
                                                     Score 80; DB 1; Length 881;
Pred. No. 0.00022;
7; Mismatches 7; Indels
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-!- MISCELLANEOUS: THIS IS AN AFRICAN MANDRILL ISOLATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Simian immunodeficiency virus (isolate GB1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11732;
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Pred. No. 0.00029;
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InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
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50.0%;
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Matches 12; Conservative
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Poly
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Best Local Similarity

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                                                                                                              13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP121)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                     E EMBL; M15390; AAB00770.1; --
R PIR; C26262; VCLJG2.
R HIV; M15390; ENV$ZROD.
R InterPro; IPR000328; Env GP41.
R InterPro; IPR000328; Env GP41.
R InterPro; IPR00517; GP120.
R Pfam; PF00516; GP120.
R Pfam; PF00517; GP41.1.
N AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
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MEDLINE-87173056; PubMed=3031510;
Guyader M., Emerman M., Sonigo P., Clavel F., Montagnier L.,
                                                                                                                                                                                          Human immunodeficiency virus type 2 (isolate ROD) (HIV-2)
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11720;
                                                                                                                                                                                                                                                                                                  "Genome organization and transactivation of the human immunodeficiency virus type 2.";
Nature 326:662-669(1987).
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                                                                                                                         Gaps
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1-0c7-1989 (Rel. 12, Last sequence update)
15-JUL-1999 (Rel. 18, Last annotation update)
15-JUL-1999 (Rel. 18, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane
11ycoprotein (GP120); Transmembrane glycoprotein (GP41)].
           (POTENTIAL).
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TRANSMEMBRANE GLYCOPROTEIN.
TRANSMEMBRANE GLYCOPROTEIN.
N-LINKED (GLCNAC. .) (POTENTIAL)
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HIV; J04498; ENV$2ISY.
INTERPRO; IPR000328; ENV GP41.
INTERPRO; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 2 (isolate SBLISY) (HIV-2). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                      -> I (IN REF. 1; AAB00770).
C7266AF1F5C5B9A7 CRC64;
                                                                                                     Length 858;
                                                                                                   Score 79; DB 1; Length 858
Pred. No. 0.0003;
7; Mismatches 7; Indels
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-!- MISCELLANEOUS: THIS ISOLATE IS FROM A GERMAN AIDS PATIENT (WITH PREDOMINANTLY NEUROLOGICAL COMPLICATIONS) WHO WAS PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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MEDLINE=90281594; PubMed=2353457;
Kirchhoff F., Jentsch K., Bachmann B., Stuke A., Laloux C.,
Lueke W., Stahl-Henning C., Schneider J., Nieselt K., Eigen M.,
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TRANSMEMBRANE GLYCOPROTEIN.
N-LINKED (GLCNAC. . . ) (POTENTIX
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
Virus—TaxID=11714;
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

protein search, using sw model OM protein - 3, 2004, 06:21:53 ; Search time 37 Seconds (without alignments) 67.594 Million cell updates/sec May Run on:

US-09-733-239-1 Perfect score:

139 1 RILAVERYLKDQQLLGIWGCSGKLIC 26 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

72

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PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1

caragraph of the protein gpl20/gp41 - human immunodeficiency virus type 1 (patient 27L) c.5pecies: human immunodeficiency virus type 1, HIV-1 c.5pecies: human immunodeficiency virus type 1, HIV-1 c.5pecies: human immunodeficiency virus type 1, HIV-1 c.5pecies: 50-reb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999 c.5Accession: 570422, 521996 c.5pecies: wildemann, B. AIDS Res. Hum. Retroviruses 8, 53-59, 1992 a.7title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb A.Reference number: 570417; MUID:92144209; PMID:1736940 a.7Accession: 570422 a.7Accession: 570422 a.7Accession: 570417; MUID:92144209; PMID:1736940 a.7Accession: 570422 a.7Accession: 570417; MUID:92144209; PMID:1736940 a.7Accession: 570422 a.7Accession: 570427 a.7Accessi \$21996

Gaps ö Length 357; Indels Query Match
100.0%; Score 139; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 26; Conservative 0; Mismatches 0;

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                                       A; Accession:
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                                                                                                                                                                                                                                                         C; Accession: S21998; S70425
R; Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Bubmitted to the EMBL Data Library, July 1991
A; Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determine ference number: S21990
                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: $21998
A;Molecule type: DNA
A;Molecule type: DNA
A;Coss-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
A;Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
A;Steuler: Hun: Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebra A;Reference number: $70417; MUD:92144209; PMID:1736940
A;Status: preliminary
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env protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S13288
R;O'Srien: W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A
Nature 348, 69-73, 1990
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
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                                                                                                                                          envelope protein gp120/gp41 - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
A;Variety: isolate 28
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: human immunodeficiency virus type 1, HIV-1
Bate: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
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R;Theodore, T.; Buckler-White, A.J.

B;Theodore, T.; Buckler-White, A.J.

B;Theodore, T.; Buckler-White, A.J.

B;Theodore, T.; Buckler-White, A.J.

B;Reference number: S54377

A;Recession: S54384

A;Status: Preliminary

A;Rolecule type: genomic RNA

A;Residues: 1-853 <THE>

A;Residues: 1-853 <THE>

C;Superfamily: type E retrovirus env polyprotein

C;Superfamily: type E retrovirus env polyprotein
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100.0%; Score 139; DB 2;
Best Local Similarity 100.0%; Pred. No. 5.2e-13;
Matches 26; Conservative 0; Mismatches 0;
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Pred. No. 2.1e-13;
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100.0%; Score 139; Dest Local Similarity 100.0%; Pred. No. 2.1
Matches 26; Conservative 0; Mismatches
RILAVERYLKDQQLLGIWGCSGKLIC 105
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C; Accession: D26192

R; Stinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu Gene 52, 71-82, 1987
A; Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti A; Reference number: A26192; MUID:87248097; PMID:3036660
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F; 801-855/Rroduct : transmembrane glycoprotein #status predicted <PWM
F; 801-855/Rroduct : transmembrane glycoprotein #status predicted <PWM
F; 801-855/Rroduct : transmembrane glycoprotein #s
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K;Keywords AIDS; capsid protein; coat protein; protein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
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N,Alternate names: coat polyprotein
C,Species: human immunodeficiency virus type 1, HIV-1
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N;Alternate names: coat polyprotein
C:Species: human immunodeficiency virus Zr-6
C:Species: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
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C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
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A; Reference number: S13288; MUID: 91043044; PMID: 2172833
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Pred. No. 5.2e-13;
; Mismatches 0;
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100.0%; Pred. No. 5.3e-13;
tive 0; Mismatches 0;
                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-854 <OBR>
C;Superfamily: type E retrovirus env polyprotein
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R; Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Call 40, 90-17, 1985
R; Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Call 40, 90-17, 1985
R; Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Call 40, 90-17, 1985
R; Rickerence number: A90866; MuID:85099333; PMID:2981635
R; Reference number: A90866; MuID:85099333; PMID:2981635
R; Genetics: A, Genetics: 
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A,Note: host Home suplement the type 1, miv-1
C,Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C,Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C,Accession: A037974
A,Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovi
A,Reference number: A93355; MUD:85111157; PMID:2982104
A,Molecule type: DNA
A,Molecule type: Allogoment type: Allog
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'Keywords: AIDS, capsid protein, coat protein, glycoprotein, immunodeficiency; polyprot
'1-30/Domain: signal sequence #status predicted <SIG>
'31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
'512-856/Product: transmembrane glycoprotein #status predicted <TWN-
'512-856/Product: transmembrane glycoprotein #status predicted <TWN-
'88-136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,386,392,397,406
'611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
F;512-856/Product: transmembrane glycoprotein #status predicted <TMM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predid
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C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A03975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: human immunodeficiency virus type 1, HIV-1
Note: host Homo sapiens (man)
Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
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                                                                                                                                                                                                              Length 856;
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                                                                                                                                                                                                                   Score 139; DB 1;
Pred. No. 5.3e-13;
                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56
                                                                                                                                                                                                                                                                                                                                                                                                                            1 RILAVERYLKDQQLLGIWGCSGKLIC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            env polyprotein precursor - human im
N;Alternate names: coat polyprotein
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100.0%;
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100.0%;
Best Local Similarity 100.0%;
Matches 26; Conservative 0
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Matches 26; Conservative
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envelope protein gp120/gp41 - human immunodeficiency virus type 1

C;Species: human immunodeficiency virus type 1, HIV-1

A;Variety; isolate 27B

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000

C;Accession: S21994; S70421

R;Stenler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A;Reference number: S21990
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                                                                                                                                                                                                                                                                                               envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
                                                                                                                                                                                                                                                                                                            C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: $70420; $22006
A;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immunodeficiency virus type 1 in bloo A;Reference number: $70417; MUID:92144209; PMID:1736940
                                                    Gaps
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A;Residues: 1-357 <ST2>
A;Cross-references: EMBL:X61354; NID:g60190; PIDN:CAA43620.1; PID:g60191
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A;Residues: 1-357 <STE1>
A;Cross-references: EMBL:X61355; NID:960179; PIDN:CAA43622.1; PID:960180
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                                                    Indels
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A;Title: Distinct populations of human immunodeficiency A;Reference number: S70417; MUID:92144209; PMID:1736940
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                        5.3e-13;
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A, Note: submitted to the EMBL Data Library, July 1991
C, Superfamily: type E retrovirus env polyprotein
DB 1;
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Pred. No. 3e-13;
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Pred. No. 3e-13;
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C;Superfamily: type E retrovirus env polyprotein
ch 100.0%; Score 139; D
1 Similarity 100.0%; Pred. No. 5.3
26; Conservative 0; Mismatches
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                                                                                                                                       1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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96.2%;
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Virology 168, 79-89, 1989
A;Title: Biological and molecular characterization of human immunodeficiency virus (HIV-
A;Reference number: A94389; MUID:89085613; PMID:2789516
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C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
F;1-29/Domain: signal sequence #status predicted <SIG>
F;3-29/Domain: coat protein gp120 #status predicted <CP1>
F;521-856/Product: coat protein gp41 #status predicted <CP2>
F;684-705/Domain: transmembrane #status predicted <TMN>
F;87,132,138,152,156,183,198,242,263,277,294,302,339,393,398,402,411,448,461,462,465,611
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R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library. July 1991
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi A;Reference number: $21990
A;Accession: $21990
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R, Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, AIDS Res. Hum. Retroviruses 5, 121-129, 1989
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N,Alternate names: coat polyprotein
                                                                                                                                                                                                                                                                                                                                                            transmembrane protein
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C;8pecies: human immunodeficiency virus type 1, HIV-1
A;Variety: isolate 20
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
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A;Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176
A;Cross-references: EMBL:X61357; PID:g60175; PIDN:CAA43626.1; PID:g60176
A;Cross-references: EMBL:X61357; PID:g60175; PIDN:CAA43626.1; PID:g60176
A;Cross-references: EMBL:X61357; PID:g60175; PID:g60176
A;Cross-references: EMBL:X61357; PID:g60175; PID:g60176
A;Cross-references: EMBL:X61357; PID:g60175; PID:g60176
A;Cross-references: EMBL:X61357; PID:g60175; PID:g60176
A;Cross-references: EMBL:X61357; PID:g60176
A;Cross-re
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                                                                                                                                     A/Accession: A31667
A;Molecule type: DNA
A;Rosidues: 1-852 <ANA>
C;Superfamily: type E rerovirus env polyprotein
C;Keywords: capsid protein; coat protein; polyprotein; F;1-516/Product: coat protein gp120 #status predicted <CP1>
F;517-852/Product: coat protein gp41 #status predicted <CP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contains: coat protein gp120; coat protein gp41; Species: human immunodeficiency virus type 1, HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.3%; Score 138; DB 1;
96.2%; Pred. No. 7.4e-13;
iive 1; Mismatches 0;
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96.2%; Pred. No. 1.1e-12;
tive 1; Mismatches 0;
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Best Local Similarity 96.2
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 25; Conserv
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R; Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
S; Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A; Reference number: $21990
A; Reference number: $21990
A; Reference number: $21900
A; Residues: 1-357 <STE1>
A; Reference number: $70417; MUD:92144209; PMID:1736940
A; Accession: $70419
A; Accession: S70419
A; Accession: S70419
A; Accession: A; Accession
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Cispecies: human immundeficiency virus type 1, HIV-1
Cispecies: human immundeficiency virus type 1, HIV-1
Cispecies: human immundeficiency virus type 26-Aug-1999
Ciscession: $70424; $21992
Ristenler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immundeficiency virus type 1 in blood and cerebra A;Reference number: $70417; MUID:92144209; PMID:1736940
A;Reference number: $70417; MUID:92144209; PMID:1736940
A;Retus: preliminary
A;Residues: 1-357 csT2>
A;Cross-references: EMBL:X61358; NID:g60177; PIDN:CAA43628.1; PID:g60178
A;Experimental source: patient 22
A;Note: submitted to the EMBL Data Library, July 1991
C;Superfamily: type E retrovirus env polyprotein
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NyAlternate names: coat polyprotein
NyAlternate names: coat protein gp120; coat protein gp121
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: host Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Feb-1997
C;Accession: A31667
R;Ahand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar,
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C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
                                                                                                                                                                                        /Variety: isolate 48
Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
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Pred. No. 3e-13;
1; Mismatches
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A;Cross-references: EMBL:X61353; NID:960188
C;Superfamily: type E retrovirus env polyprotein
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Local Similarity 96.2%;
nes 25; Conservative
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Matches 25; Conservative
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Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebri
Reference number: S70417; MUID:92144209; PMID:1736940
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C;Species: human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C;Accession: $22000
E;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determiny A;Reference number: $21990
A;Reference number: $21900
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-358 <STF>
A;Residues: 1-358 <STF>
A;Cross-references: EMBL:X61351
C;Superfamily: type E retrovirus env polyprotein
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C;Species: human immunodeficiency virus type 1, HIV-1
A;Variety: isolate 3L
C;Dete: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
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                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-332,'X',334-357 <STE2>
A;Residues: 1-332,'X',334-357 <STE2>
A;Cross-references: EMBL:X61357; NID:g60175; PIDN:CAA43626.1; PID:g60176
C;Superfamily: type E retrovirus env polyprotein
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Best Local Similarity 92.3%; Pred. No. 8.7e-13;
Matches 24; Conservative 2; Mismatches 0;
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envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragmen CiSpecies: human immunodeficiency virus type 1, HIV-1
A'Variety: patient 3B
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C;Accession: S70417
R;Stenler, H.; Storch-Hagenlocher, B.; Wildemann, B.
Alba Res. Hum. Retroviruses 8, 53-59, 1992
A;Fitle: Distinct populations of human immunodeficiency virus type 1 in blood and cereb A;Reference number: S70417; MUD:92144209; PMID:1736940
A;Accession: S70417
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-358 <STE>
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A;Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity A;Reference number: A41621; MUID:92107924; PMID:1763038
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F;252-443/Product: coat protein gp10 (fragment) #status predicted <GP2>
F;252-443/Powain: transmembrane #status predicted <TMN>
F;424-443/Powain: transmembrane #status predicted <TMN>
F;9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,357/Binding site: c
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N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C;Species: human immunodeficiency virus type 1, HIV-1
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C;Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C;Accession: C41621
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A,Rebidues: 1-443 - SBUA.
A,Rebidues: 1-443 - SBUA.
A,Cross-references: GB:M77230; NID:g328631; PIDN:AAB03792.1; PID:g555015
A,Note: this virus was isolated from the mother's sexual partner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 358;
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Pred. No. 8.7e-13;
2; Mismatches 0; Indels
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C;Species: human immunodeficiency virus type i, HIV-1
C;Species: human immunodeficiency virus type i, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T12016
R;McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998
A;Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S; A;Reference number: Z17379; MUID:9817816; PMID:9519894
A;Accession: T12016
A;Accession: T12016
A;Accession: Draininary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-852 ACCC
A;Cross-references: EMBL:U90934; NID:g2351783; PIDN:AAC59271.1; PID:g2351784
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N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Accession: A03976
C;Accession: A03976
C;Accession: A03976
S;Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Si Science 227, 484-492, 1985
A;Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;738-755/Domain: transmembrane #status predicted <TMN>
F;87,129,135,138,134,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435
                                                                                                                                                               R.Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M. J. Virol. 66, 6587-6600, 1992 encue.
A,Title: Complete nucleotide sequence, genome organization, and biological properties A,Reference number: A44001; NUID:93021387; PMID:1404605
A,Accession: H44001
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C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1994
C;Accession: H44001
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Pred. No. 2.1e-12;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.1%; Score 135; DB 1; Length 843; 92.3%; Pred. No. 2.1e-12; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: coat protein; glycoprotein; polyprotein; transmer F;12-91/Domain: signal sequence #status predicted <SIG>F;12-95/Domain: signal sequence #status predicted <SIG>F;19-35/Region: hydrophobic F;30-489/Product: coat protein gp120 #status predicted <GP1>F;30-843/Product: coat protein gp41 #status predicted <GP2>F;49-515/Region: hydrophobic F;673-689/Region: hydrophobic
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C, Superfamily: type E retrovirus env polyprotein
C, Superfamily: type E retrovirus env polyprote
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92.3%;
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Matches 24; Conservative
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Best Local Similarity 92.37
Marches 24, Conservative
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A, Residues: 1-843 <LIY>
A, Cross-references: GB:M93258
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VCLJA2
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T12016
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             N; Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120 C; Species: human immunodeficiency virus type 1, HIV-1 A; Note: host thomo sapiens (man) C; Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999 C; Accession: A41621 R; Barquence_revision 31-Dec-1993 #text_change 26-Aug-1999 C; Accession: A41621 R; Barquence_revision 31-Dec-1993 #text_change 26-Aug-1999 C; Accession: A41621 A; Bs, 11236-11240, 1991 D; Note: Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991 N; Gibbs, R.A. A; Reference number: A41621; MUID: 92107924; PMID: 1763038 A; Reference number: A41621; MUID: 92107924; PMID: 1763038 A; Residues: 1-445 <BUR>
A; Residues: 1-445 <BUR>
A; Residues: 1-445 <BUR>
A; Residues: 1-445 <BUR>
A; Residues: 1-45 <BUR>
A; Residues: 1-445 \Broadic: coat protein; gp41 (fragment) #statue predicted <GP2>
F; 255-4445 / Domain: transmembrane #status predicted <TMN>
F; 255-445 / Domain: transmembrane #status predicted <TMN>
F; 25, 19, 23, 42, 48, 78, 85, 101, 107, 131, 137, 143, 147, 152, 155, 190, 205, 353, 358, 367, 379/Binding site:
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R;Burger, H.; Weiser, B.; Plaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Procession: Sci. U.S.A. 88, 11236-11240, 1938
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1938
A;Title: Evolution of human immundeficiency virus type 1 nucleotide sequence diversity
A;Reference number: A41621; MUID:92107924; PMID:1763038
A;Recession: B41621
A;Molecule type: DNA
A;Residues: 1-454 *BUR>
A;Residues: 1-454 *BUR>
A;Cross-references: GB:M77279
A;Note: this virus was isolated from the daughter
C;Genetics:
A;Genetics:
A;G
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N;Alternate names: coat polyprotein
N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C;Species: human immunodeficiency virus type 1, HIV-1
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C;Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 31-Jan-1997
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97.1%; Score 135; DB 2; Length 445;
Best Local Similarity 92.3%; Pred. No. 1.1e-12;
Matches 24; Conservative 2; Mismatches 0; Indels
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Pred. No. 1.1e-12;
2; Mismatches 0;
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92.3%;
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Best Local Similarity
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H44001
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A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prot
C;Keywords: apsid protein; coat protein; glycoprotein; polyprotein; transmembrane prot
F;1-29/Domain: signal sequence #status predicted <BPP>
F;30-861/Product: env polyprotein #status predicted <EPP>
F;87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribesai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, Proc. Natl. Acad. Sci. US.A. 38, 8380-8384, 1986
Proc. Natl. Acad. Sci. US.A. 38, 8380-8384, 1986
A;Title: Molecular cloning and primary nucleociide sequence analysis of a distinct human
A;Reference number: A94136; MUID:87041461; PMID:3490666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prot
F;1521/Product: coat protein gp10 #status predicted <GP2>
F;522-868/Product: coat protein gp41 #status predicted <GP2>
F;89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,45
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R,Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-St R,Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-St V, Kology, 164, 531-536, 1988
A;Title: Envelope sequences of two new United States HIV-1 isolates.
A;Reference number: A28922; WUID:88219542; PMID:3369091
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C; Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prot:
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-859/Product: env polyprotein #status predicted <EPP>
F;87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401
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N;Alternate names: coat polyprotein
N;Contains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 30-7un-1988 #sequence_revision 30-7un-1988 #text_change 16-Jul-1999
C;Accession: C25523
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C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec.1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
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A; Molecule type: DNA
A; Reaidues: 1-868 < DES>
A; Cross-references: GB:M13137; NID:g326460; PIDN:AAA44311.1; PID:g326467
C; Genetics:
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                                                                                                                                                                                                                                                                     97.1%; Score 135; DB 1; Length 861; 92.3%; Pred. No. 2.2e-12; ive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                             Query Match
Best Local Similarity 92.3%
----hem 24; Conservative
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A;Molecule type: DNA
A;Residues: 1-859 <GUR>
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A;Molecule type: DNA
A;Residues: 1-856 <STA>
A;Residues: 1-856 <STA>
A;Coss_references: GB:K03455; GB:M38432; NID:g1906382
C;Genetics:
A;Genetics:
A;Genetics: A;Genetics: GB:K03455; GB:M38432; NID:g1906382
C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: Gat protein; glycoprotein; polyprotein; transmembrane protein
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <GF1>
F;30-501/Product: coat protein gp41 #status predicted <GF2>
F;502-847/Product: coat protein gp41 #status predicted <GF2>
F;802-847/Product: C34,241,262,276,289,295,331,338,354,360,399,404,447,459
                                                                                            A;Residues: 1-855 <SAN>
A;Cross-references: GB:K02007; NID:g328658; PIDN:AABS9882.1; PID:g328666
C;Genetics:
A;Gene: car.
A;Gene: car.
C;Genetics:
A;Gene: capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote; C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote; E71-30/Domain: signal sequence #status predicted <SIG>
F;13-50/Porduct: exterior membrane glycoprotein #status predicted <EXT>
F;31-50/Domain: glycoprotein; mstatus predicted <TMM>
F;510-855/Product: transmembrane glycoprotein; mstatus predicted <TMM>
F;610,652,140,158,184,190,200,244,265,292,298,304,341,358,364,388,394,400,408,445,458
F;610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted
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NyAlternate names: coat polyprotein
A.Note: host Homo saplens (man)
C.Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C.Accession: B28922
NyTology 164, 531-536, 1988
A.Title: Envelope sequences of two new United States HIV-1 isolates.
A.Reference number: A28922, MUID:88219542; PMID:3369091
A.Recession: B28922
A.Rocession: B28922
A.Rocession: B28922
A.Rocession: B28922
A.Rocession: C. GUR
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R; Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, A; Fille: Identification and characterization of conserved and variable regions in the A; Reference number: A24774; MUID:86218077; PMID:2423250
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Species: human immunodeficiency virus type 1, HIV-1
Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
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97.1%; Score 135; DB 1; Length 856;
Best Local Similarity 92.3%; Pred. No. 2.2e-12;
Matches 24; Conservative 2; Mismatches 0; Indels
A; Reference number: A04003; MUID:85090453; PMID:2578227
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Matches 24; Conservative
                                                                                DNA
                                    ;Accession: A03976
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C;Superfamily: type E retrovirus env polyprotein
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
E;1-689/Domain: satractus predicted <EXT>
F;1-33/Domain: signal sequence #status predicted <EXT>
F;1-33/Domain: signal sequence #status predicted <IG>F;17-33/Region: hydrophobic #status predicted
F;34-517/Region: cleavage processing #status predicted
F;514-517/Region: cleavage processing #status predicted
F;518-534/Region: hydrophobic #status predicted <IMI>F;690-711/Domain: intracellular #status predicted <IMI>F;712-861/Domain: intracellular #status predicted <IMI>F;712-861/Domain: hydrophobic #status predicted
F;756-772/Region: hydrophobic #status predicted
F;756-772/Region: hydrophobic #status predicted
F;93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,408,414,
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R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submitted to the EMBL Data Library, July 1996
A;Reference number: Z16673
A;Accession: T09448
                                                                                                                                                                                                                                                                                                                                         C;Accession: A42995
R;Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992
A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
A;Reference number: A42995, MUID:92351552; PMID:1322587
                                                                                                            immunodeficiency virus type 1 (strain KB-1-gp41)
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                                                                                                        env polyprotein precursor - human immunodeficiency virus type , (strain no-laborate names: coat polyprotein N;Contains: coat protein gp120; coat protein gp41 (Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C;Bpecies: al-Mar-1993 #sequence_revision 31-Mar-1993 #sequence_revision 31-Mar-1999 #text_change 01-Mar-1996
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
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Pred. No. 6.2e-12;
2; Mismatches 1; Indels
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Pred. No. 8.7e-12;
1; Mismatches 1; Indels
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A;Residues: 1-847 <PAN>
A;Cross-references: EMBL:U63632; NID:91465777; PID:91465781
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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S13289
env protein - human immunodeficiency virus type 1
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C,Superfamily: type E retrovirus env polyprotein
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A;Cross-references: GB:S41266; GB:D01206
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ilarity 92.3%;
Conservative
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Best Local Similarity 88.5
Matches 23; Conservative
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Best Local Similarity
Matches 24; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                          Any Polyprocein precursor - numan immunodericiency virus type 1 (strain KB-1-9922)

N.Alternate names: coat polyprotein
N.Contains: coat protein gp120; coat protein gp32
C.Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996
C;Accession: 842995
R;Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992
A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated A;Accession: B42995
A;Accession: B42995
A;Accession: B42995
A;Molecule type: mANA
C;Genetics:
A;Conetics:
A;Gene: env
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein; transmembrane protein
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
C;Keywords: coat protein gp120 #status predicted <CP1>F;1-33/Region: cleavage processing #status predicted <CP2>F;1-34/Region: cleavage processing #status predicted <CP2>F;1-35/Region: cleavage processing #status predicted <CP2>F;1-151/Region: cleavage processing #status predicted <CP2>F;11-51/Region: cleavage processing #status p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F.17-37/Region: hydrophobic #status predicted <CPl>
F.34-517/Region: hydrophobic #status predicted <CPl>
F.34-517/Region: cleavage processing #status predicted <CPl>
F.514-517/Region: cleavage processing #status predicted <CP2>
F.518-729/Product: cat procein gp32 #status predicted <CP2>
F.518-534/Region: hydrophobic #status predicted <CP2>
F.509-711/Domain: transmembrane #status predicted <TM1>
F.712-729/Domain: intracellular #status predicted <TM7>
F.93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,338,345,361,367,397,403,408,414
                                                                                                                                                                                                                                                                                                                                                                                         - human immunodeficiency virus type 1 (strain KB-1-gp32)
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar.1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C;Accession: S33985
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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C. Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1997
C. Accession: 833985
C. Accession: 833985
C. Accession: 833985
C. A. Reference number: 833979
A. Reference number: 833979
A. Accession: 833985
A. Status: preliminary
A. Status: preliminary
A. Residues: 1-851 c CAR>
A. Residues: 1-851 c CAR>
A. Cross-references: EMBL: 211530; NID:g60192; PIDN:CAA77628.1; PID:g60199
C. Superfamily: type E retrovirus env polyprotein
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Best Local Similarity 96.2%; Pred. No. 6.2e-12;
Matches 25; Conservative 0; Mismatches 1; Indels
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 95.0%; Score 132; DB Best Local Similarity 88.5%; Pred. No. 5.2e Matches 23; Conservative 2; Mismatches
                                        1; Mismatches
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                                                                                                                                                                    574 RILAVERYLKDQQLLGIWGCSGKPIC 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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    Pred.
Best Local Similarity 92.3%;
Matches 24; Conservative 1
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C;Keywords: AlDS; capsid protein, contribution; glycoprotein, immunodeficiency; polyprorefiles and sequence #status predicted <SIS>
Fil-30/Domain: signal sequence #status predicted <CPI>
Fish-50/Product: coat protein gp120 #status predicted <CPI>
Fish-854/Product: coat protein gp14 #status predicted <CPI>
Fish-854/Product: coat protein gp41 #status predicted <CPI>
Fish-854/Product: coat protein gp41 #status predicted <CPI>
Fish-854/Product: coat protein gp41 #status predicted <CPI
Fish-854/Product: coat protein gp120 #status predicted <CPI
Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854/Fish-854
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Cell 46, 63-74, 1986
A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two iso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rivanden Haesevelde, M.; Decourt, J.L.; De Leys, R.J.; Vanderborght, B.; van der Groen, J. Virol. 68, 1586-1595, 1994
A;Title: Genomic cloning and complete sequence analysis of a highly divergent African h
A;Reference number: A53034; MUID:94149849; PMID:8107220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: human immunodeficiency virus type 1 (strain Ant70)
1Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
3Accession: A53034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: human immunodeficiency virus type 1, HIV-1
Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                        A;Cross-references: EMBL:X52154; NID:g58866; PIDN:CAA36407.1; PID:g58874
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:K03456; NID:g60228; PIDN:CAA28016.1; PID:g60234 C;Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           envelope polyprotein precursor - human immunodeficiency virus type 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 859;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
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                                                   nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Reference number: 214389; MUID:86245056; PMID:2424612
A, Accession: T01672
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80.8%; Pred. No. 4.3e-10;
tive 4; Mismatches 1;
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A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 98; DB 2;
Pred. No. 1e-06;
6; Mismatches
                                                                                                                                                                                                                                                                                                  Superfamily: type E retrovirus env polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:L02587
C;Superfamily: type E retrovirus env
C;Keywords: polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.5%;
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Best Local Similarity 75...
Best Local Similarity 75...
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Matches 21; Conservative
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Best Local Similarity 61.5
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: genomic RNA
A; Residues: 1-863 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-859 <ALI>
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A;Status: preliminary
                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: T01672
                 A;Accession: S09990
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S13289
C;Accession: S13289
Nature 348, 69-73, 1990
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gpl20
A;Reference number: S13289
A;Reference number: S13289
A;Reference number: S13289
A;Accession: S13289
A;Accession: S13289
A;Accession: Draliminary
A;Molecule type: DNA
A;Residues: 1-847 <OBR>
C;Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Note: host Homo sapiens (man)

Local Date: Josep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C.Jace: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C.Jacession: J00066

R.Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;

R.Spire, B.; 275-284, 1989

A.Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immunch;

A.Reference number: J00066; MUID:90034200; PMID:2806917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot F;1-29/Domain: signal sequence #status predicted <SIG> F;30-501/Product: coat protein gp120 #status predicted <CP1> F;502-846/Product: coat protein gp41 #status predicted <CP2> F;502-846/Product: coat protein gp41 #status predicted <CP2> F;502-850/Domain: transmembrane #status predicted <TM1> F;674-692/Domain: transmembrane #status predicted <TM2> F;87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK) N,Alternate names: coat polyprotein N;Contains: coat protein gp120; coat protein gp41 C;Species: human immunodeficiency virus type 1, HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      env polyprotein precursor - simian immunodeficiency virus SIVcpz N;Alternate names: coat polyprotein N;Contains: coat protein gp120; coat protein gp41 C;Species: simian immunodeficiency virus SIVcpz A;Note: host Pan troglodytes (chimpanzee) C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: $09990
R;Huet, T; Cheynier, R; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Mature 345, 356-359, 199
A;Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A;Reference number: $09983; WUID:90259077; PMID:2188136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Residues: 1.846 <SPI>
A) Cross-references: GB:M27323; NID:g328154; PIDN:AAA44873.1; PID:g328162
A) Cross-references: GB:M27323; NID:g328154; PIDN:AAA44873.1; PID:g328162
A) Note: the authors translated the codon GCG for residue 523 as Arg
C; Genetics:
A; Gene: env
C; Superfamily: type E retrovirus env polyprotein
C; Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodefic
F; 1-29/Domain: signal sequence #status predicted <GIS>
F; 10-50/Product: coat protein gp120 #status predicted <CPI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 131; DB 2;
Pred. No. 8.7e-12;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     570 RVLAVERYLGDQQLLGIWGCSGKLIC 595
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Local Similarity 92.3%;
hes 24; Conservative
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les 22; Conserv
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Matches
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C;Accession: H33943
R;Kumar, P.; Hui, H.; Kappes, J.C.; Haggarty, B.S.; Hoxie, J.A.; Arya, S.K.; Shaw, G.M.; Virol. 64, 890-901, 1990
A;Title: Molecular characterization of an attenuated human immunodeficiency virus type 2 A;Reference number: A33943; MUID:90112662; PMID:2296086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cikeywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F11-19/Domain: signal sequence #status predicted <SIG>
F120-501/Product: env polyprotein #status predicted <ENV>
F20-501/Product: env polyprotein gp120 #status predicted <SGG>
F506-859/Product: transmembrane glycoprotein gp21 #status predicted <TGG>
F5505-859/Product: transmembrane glycoprotein gp41 #status predicted <TGG>
F5505-859/Product: transmembrane #status predicted <TWN>
F6507-594/Domain: transmembrane #status predicted <TWN>
F365,69,78,113,119,111,137,145,160,173,186,200,232,235,235,242,266,272,283,294,304,359,392,40
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A;Reference number: A47665; MUID:94016835; PMID:8411355
A;Accession: A47665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    env polyprotein precursor - human immunodeficiency virus type 2 (isolate ST) NiAlternate names: coat polyprotein NiAlternate annes: coat polyprotein gpl20; transmembrane glycoprotein gp41 C;Species: human immunodeficiency virus type 2, HIV-2
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C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
C;Accession: A47665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: host Homo sapiens (man)
C;Date: 31-Dec_1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kodama, T.; Mori, K.; Kawahara, T.; Ringler, D.J.; Desrosiers, R.C.
J. Virol. 67, 6522-6534, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   env protein gp120(clone Mm316-85) - simian immunodeficiency virus
                                                                               A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-855 <BAR> A;Residues: 1-855 <BAR> A;Experimental source: UCl A;Note: sequence extracted from NCBI backbone (NCBIP:122362) C;Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-869 <KOD>
                                                                                                                                                                                                                                                                                                                                                                                           Length 855;
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7; Indels
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A; Reference number: A45713; MUID: 93124535; PMID: 8419635
                                                                                                                                                                                                                                                                                                                                                                                  64.0%; Score 89; DB 2; Le
ilarity 53.8%; Pred. No. 2.3e-05;
Conservative 6; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: brain isolate, Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           572 RVTAIEKYLKDQAQLNSWGCASRQVC 597
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Best Local Similarity 50.0%
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A; Residues: 1-859 < KUM>
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 14; Conserv
                                            A; Accession: A45713
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
C;Accession: S52930
B;Cohen, J.H.M.; Guetard, D.; Philbert, F.; Chamaret, S.; Tabary, T.; Montagnier, L.; de submitted to the EMBL Data Library, January 1995
A;Description: A novel HIV1-O strain illustrates the diversity of the O group.
A;Accession: S52930
A;Accession: S52930
A;Accession: S22930
A;Accession: Cs2930
A;Accession: S12930
A;Accession: S12930
A;Accession: L104 <COH:
A;Residues: 1-104 <COH:
C;Superfamily: type E retrovirus env polyprotein
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A45713
Env transmembrane protein gp43 - human immunodeficiency virus type 2
Env transmembrane protein gp43 - human immunodeficiency virus type 2
C;Species: human immunodeficiency virus type 2, HIV-2
C;Date: 04-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
C;Date: 04-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
C;Accession: A45713
R;Barnett, S.W.; Quiroga, M.; Werner, A.; Dina, D.; Levy, J.A.
J. Virol. 67, 1006-1014, 1993
A;Title: Distinguishing features of an infectious molecular clone of the highly divergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: S4919/
Appearation of the EMBL Data Library, July 1994
Appearation of the EMBL Data Library, July 1994
Appearation isolation and envelope sequence of a highly divergent HIV-1 isolate: defining the defining of the EMBL Data Library, July 1994
Appearation: Isolation and envelope sequence of a highly divergent HIV-1 isolate: defining the defining states of the defining type: DNA
Appearation: S49197
Appearation: S49
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Pred. No. 1.3e-06;
6; Mismatches 5; Indels
                                                                                            |:||:| |::||||:|
581 RLLALETLLONOOLLSLWGCKGKLVC 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:||:| ::::|||| :|||
594 RLLALETFIQNQQLLNLWGCKNRLIC 619
                                            1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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Best Local Similarity 57.7%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                           RESULT 38
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R,Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.; Nature 358, 495-499, 1992
Nature 358, 495-499, 1992
A;Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa. A;Reference number: S30448; MUID:92350299; PMID:1641038
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C;Date: 02-Dec-1993 #sequence revision 30-Jan-1998 #text_change 17-Mar-1999
C;Accession: S30448; S30480; S30480;
R;Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
Nature 358, 495-499, 1992
A;Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
A;Reference number: S30448; MUID:92360299; PMID:1641038
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A,Experimental source: FOENVA3
A,Experimental source: FOENVA3
A,Experimental source: FOENVA3
S,Fao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.; submitted to the EMBL Data Library, December 1992
A,Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Afric
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                                                                env protein - human immunodeficiency virus type 2 (fragment)
C;Species: human immunodeficiency virus type 2, HIV-2
C;Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999
C;Accession: S30459
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50.0%; Pred. No. 3.2e-05;
Migmarches 7;
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C,Superfamily: type E retrovirus env polyprotein
C,Keywords: coat protein; glycoprotein
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A, Residues: 1-151 <GAO>
A, Cross-references: EMBL: M87069
A, Experimental Bource: FOENVAl3
A, Accession: S30449
A, Status: preliminary; translation not shown
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23 RVTAIEKYLKDQAQLNSWGCAFRQVC 48
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50.0%;
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A;Molecule type: nucleic acid
A;Residues: 1-151 <GAO>
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C; Genetics:
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A;Accession: S30481
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Best Local Similarity 50.09
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A; Residues: 1-151 <GAW>
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A; Residues: 1-151 <GA2>
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Matches
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C;Species: human immunodeficiency virus type 2, HIV-2
C;Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 23-Mar-2001
C;Accession: 830458, 830477
R;Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
Asture 358, 495-499, 1992
A;Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
A;Reference number: 830448; MUID:92350299; PMID:1641038
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A; Molecule type: nucleic acid
A; Residues: 1-151 <GAO>
A; Cross-references: EMBL:M87142
A; Cross-references: EMBL:M87142
A; Cross-references: EMBL:M97142
A; Cao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.; submitted to the EMBL Data Library, December 1992
A; Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa
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Nature 300, 184-186, 1987
A;Title: Relation of HTLV-4 to simian and human immunodeficiency-associated viruses. A;Title: Reference number: 803068
A;Reference number: 803068
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-881 - HAH>
A;Residues: 1-881 - HAH>
A;Residues: 1-881 - HAH>
A;Crosssreferences: EMBL:X06391
A;Crossreferences: EMBL:X06391
A;Crossreferences: EMBL:X06391
C;Superfamily: type E retrovirus env polyprotein
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;Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 03-May-1996
                                                                   Gaps
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      Length 869;
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   Score 84; DB 2; Length 869
Pred. No. 0.00014;
6; Mismatches 7; Indels
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Best Local Similarity 50.0%; Pred. No. 3.2e-05;
Matches 13; Conservative 6; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                   protein - human T-cell lymphotropic virus type 4
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A;Accession: $30477
A;Status: preliminars
A;Molecule type: nucleic acid
A;Residues: 1-151 cGA2>
A;Cross-references: EMBL:M87141
A;Genetics:
A;Genetics:
A;Genetics: C;Superfamily: type E retrovirus env polyprotein
C;Keywords: coat protein; glycoprotein
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594 RVTAIEKYLKDQAQLNTWGCAFRQVC 619
                                                                                                                       1 RILAVERYLKDQQLLGIWGCSGKLIC 26
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Query Match 60.4%;
Best Local Similarity 50.0%;
Matches 13; Conservative
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Length 151;

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R;Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.; Nature 358, 495-499, 1992
A;Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa. A;Reference number: S30448; MUID:92350299; PMID:1641038
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C;Species: human immunodeficiency virus type 2, HIV-2
C;Species: human immunodeficiency virus type 2, HIV-2
C;Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999
C;Accession: S30457
R;Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M. Mature 358, 495-499, 192
A;Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
A;Reference number: S30448; MUID:92350299; PMID:1641038
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C,Species: human immunodeficiency virus type 2, HIV-2
C,Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999
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Pred. No. 3.2e-05;
6; Mismatches 7; Indels
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Pred. No. 3.2e-05;
6; Mismatches 7; Indels
A,Reference number: S30448; MUID:92350299; PMID:1641038
A,Accession: S30450
A,Status: translation not shown
A,Wolecule type: nucleic acid
A,Residues: 1-151 <GAO>
A,Cross-references: EMBL:M87072
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Best Local Similarity 50.0%; Pred. No. 3.2e-05;
Matches 13; Conservative 6; Mismatches 7;
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C;Superfamily: type E retrovirus env polyprotein
C;Keywords: coat protein; glycoprotein
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C;Superfamily: type E retrovirus env polyprotein
C;Keywords: coat protein; glycoprotein
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23 RVTAIEKYLKDQAQLNSWGCAFRQVC 48
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illarity 50.0%;
Conservative 6
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Best Local Similarity 50.0%;
Matches 13; Conservative
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A;Molecule type: nucleic acid
A;Residues: 1-151 cGAO>
A;Cross_references: EMBL:M87130
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A;Molecule type: nucleic acid
A;Residues: 1-151 cGAO>
A;Cross-references: EMBL:M97074
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Matches 13; Conserv
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C;Species: human immunodeficiency virus type 2, HIV-2
C;Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999
C;Dates: 02-bec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999
R;Gao, F: vec, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
Nature 358, 495-499, 1992
A;Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rigor, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.; Nature 358, 495-499, 1992
A;Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa. A;Reference number: S30448; MUID:92350299; PMID:1641038
A;Accession: S30453
A;Status: translation not shown
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Residues: 1-151 <GAO>
A;Residues: 1-151 <GAO>
A;Conetics:
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C;Species: human immunodeficiency virus type 2, HIV-2
C;Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999
C;Accession: S30452
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Pred. No. 3.2e-05;
6; Mismatches 7; Indels
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Pred. No. 3.2e-05;
6; Mismatches 7; Indels
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C,Superfamily: type E retrovirus env polyprotein
C,Keywords: coat protein; glycoprotein
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23 RVTAIEKYLKDQAQLNSWGCAFRQVC 48
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Best Local Similarity 50.0%;
Matches 13; Conservative (
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Best Local Similarity 50.0%;
Matches 13; Conservative
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env protein - human immunodeficiency virus type 2 (fragment)
Cispecies; human immunodeficiency virus type 2, HIV-2
Cispecies; human immunodeficiency virus type 2, HIV-2
Cidate: 09-May-1997 #sequence_revision 09-May-1997 #text_change 17-Mar-1999
CiAccession: 830465; 830460; 830463; 830464; 830464; 830466; 830467; 830468; 830470; 83
RiGao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
Albescription: Human infection by genetically diverse SIVSM-related HIV-2 in west Afric
A;Reference number: 830460
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A; Residues: 1-151 <GAC>
A; Cross-references: EMBL:W87125
A; Experimental sources: Clone 22ENVBB2
R; Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
Ryture 358, 495-499, 1992
A; Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
A; Reference number: S30448; MUID:92350299; PMID:1641038
   23 RVTAIEKYLKDQAKINSWGCAFRQVC 48
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A;Experimental source: clone 22ENVB15
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A;Accession: 830464
A;Molecule type: nucleic acid
A;Residues: 1-151 cGAZ>
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A;Experimental source: clone 22ENVB17
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;Experimental source: clone 22ENVBB4
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Experimental source: clone 22ENVBB1
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A, Accession: $30463
A, Molecule type: nucleic acid
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Experimental source: clone 22ENVB5
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A,Cross-references: EMBL:M87132
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A;Molecule type: nucleic acid
A;Residues: 1-151 <GAW>
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R;Gao, F; Yue, L; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
Mature 318, 495-499, 1992
A;Title: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
A;Reference number: $30448; MUID:92350299; PMID:1641038
A;Accession: $30456
A;Accession: $30456
A;Status translation not shown
A;Molecule type: nucleic acid
A;Residues: 1-151 <GAO>
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A, Status: Lanslation not shown
A, Molecule type: nucleic acid
A, Residues: 1-151 (GAO)
A, Residues: 1-151 (GAO)
A, Residues: 1-151 (GAO)
A, Cross-references: EMBL:M87123
B, GAO, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.; submitted to the EMBL Data Library, December 1992
A, Poscription: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa A, Accession: S30460
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C.Species: human immunodeficiency virus type 2, HIV-2
C.Species: human immunodeficiency virus type 2, HIV-2
C.Date: 02-Dec-1993 #sequence revision 30-Jan-1998 #text_change 23-Mar-2001
C.Accession: 830455, 830461, §30469
R.Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
Astrile: Human infection by genetically diverse SIV(SM)-related HIV-2 in West Africa.
A.Reference number: 830448; MUID:92350299; PMID:1641038
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C;Species: human immunodeficiency virus type 2, HIV-2
C;Date: 02-Dec-1993 #sequence_revision 30-Jan-1998 #text_change 17-Mar-1999
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Pred. No. 3.2e-05;
6; Mismatches 7; Indels
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Pred. No. 3.2e-05;
6; Mismatches 7; Indels
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C,Superfamily: type B retrovirus env polyprotein
C,Keywords: coat protein; glycoprotein
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1 RILAVERYLKDQQLLGIWGCSGKLIC 26
|: |: |: || || || || || || 23 RVTAIEKYLKDQAKLNSWGCAFRQVC 48
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A;Molecule type: nucleic acid
A;Residues: 1-151 <GA2>
A;Cross-references: EMBL:M87131
A;Accession: 830469
A;Status: preliminary
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Best Local Similarity 50.0%;
Matches 13; Conservative
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A, Molecule type: nucleic acid
A, Residues: 1-151 <GA3>
A, Cross references: EMBL: M87122
C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:M87129
C;Genetics:
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Best Local Similarity 50.0%
Matches 13; Conservative
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1 RILAVERYLKDQQLLGIWGCSGKLIC 26

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us-09-733-239-1.rpr

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F;20-712/Product: env polyprotein #status predicted <ENV>
F;20-501/Product: surface glycoprotein gpl20 #status predicted <SGG>
F;506-712/Product: transmembrane glycoprotein gp41 #status predicted <TPG>
F;507-523/Region: hydrophobic
F;675-694/Pomain: transmembrane #status predicted <TMN>
F;675-694/Pomain: tran
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A;Variety: isolate SAB-1
C;Date: 25-Dec-1994 #sequence_revision 14-Feb-1997 #text_change 20-Sep-1999
C;Accession: 346352
B;Jin, M.J.; Hul, H.; Robertson, D.L.; Mueller, M.C.; Barre-Sinoussi, F.; Hirsch, V.M.; BiMBO J. 13, 2935-2947, 1994
A;Title: Mosaic genome structure of simian immunodeficiency virus from West African gree A;Accession: 346352
A;Accession: 346352
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R;Kuehnel, H.; Kreutz, R.; Ruebsamen-Waigmann, H.
R;Kuehnel, H.; Kreutz, R.; Ruebsamen-Waigmann, H.
Nucleic Acids Res. 18, 6142, 1990
A;Title: Nucleotide sequence of HIV-2(D194), an isolate from a Gambian case of 'Neuro-AI)
A;Reference number: S12152; MUID:91045094; PMID:2235509
A;Accession: S12159
A;Acce
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A;Cross-references: BMBL:U04005; NID:g466229; PIDN:AAA21510.1; PID:g466236
A;Cross-references: BMBL:U04005; NID:g466229; A;Cross-references: BMBL:U04005; NID:g466236
A;Cross-references: BMBL:U04005; NID:g466229; PIDN:AA21510.1; PID:g466236
A;Cross-references: BMBL:U04005; NID:g466229; PIDN:AA21510.1; PID:g466236
A;Cross-references: BMBL:U04005; NID:g466229; PIDN:AA21510.1; PID:g466236
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1990
C;Superfamily: type E retrovirus env polyprotein
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C,Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
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50.0%; Pred. No. 0.00016;
iive 6; Mismatches 7; Indels
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C,Superfamily: type E retrovirus env polyprotein
C,Keywords: capsid protein; coat protein; polyprotein
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6; Mismatches
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594 RVTALEKYLEDQARLNIWGCAFRQVC 619
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Matches 13; Conservative
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Best Local Similarity
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NyAlternate names: coat polyprotein
NyAlternate names: coat polyprotein
NyAlternate names: coat polyprotein
NyAlternate names: coat polyprotein
C;Species: simian immunodeficiency virus, SIV
A;Note: host Macaca arctoides (stump-tailed macaque)
C;Date: l2-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 26-Aug-1999
C;Accession: B41565
B;Khan, A.S.; Galvin, T.A.; Lowenstine, L.J.; Jennings, M.B.; Gardner, M.B.; Buckler, C.
J, Virol. 65, 7061-7065, 1991
A;Title: A highly divergent simian immunodeficiency virus (SIVstm) recovered from stored A;Reference number: A41565; MUID:92046379; PMID:1942258
A;Molecule type: DNA
A;Residues: 1-366 KHA>
A;Cross-references: GB:X60668; NID:g60525; PIDN:CAA43085.1; PID:g60526
C;Genetics:
A;Genetics:

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C;Superfamily: type E retrovirus env polyprotein
C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
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Pred. No. 8.1e-05;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                Score 83; DB 2; Length 13. Pred. No. 3.2e-05;
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7; Indels
                                                             A;Molecule type: nucleic acid
A;Residues: 1-151 cGA2>
A;Cross-references: EMBL:M07118
C;Superfamily: type E retrovirus env polyprotein
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Best Local Similarity 50.0%;
Matches 13; Conservative
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Best Local Similarity 50.0%;
Matches 13; Conservative
           A; Accession: S30454
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env polyprotein - simian immunodeficiency virus (macaque isolate)
C;Species: simian immunodeficiency virus, SIV
C;Species: olun-1989 #sequence_revision 30-Jun-1989 #text_change 07-Nov-1997
C;Accession: H28887
R;Chakrabarti, L.; Guyader, M.; Alizon, M.; Daniel, M.D.; Desrosiers, R.C.; Tiollais, P. Nature 328, 543-547, 1987
Nature 328, 543-547, 1987
A;Title: Sequence of simian immunodeficiency virus from macaque and its relationship to A;Reference number: A28887; MUID:87287230; PMID:3649576
A;Accession: H28887
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C;Superfamily: type B retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; immunodeficiency; polyprotein; transmem
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       env protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Peb-1995 #sequence_revision 20-Peb-1995 #text_change 26-Aug-1999
C;Accession: S24571
R;Dietrich, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Species: human immunodeficiency virus type 2, HIV-2
C,Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-869 <BEC>
A;Cross-references: EMBL:Z48731; NID:g732718; PIDN:CAA88627.1; PID:g732726
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: polyprotein
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A;Residues: 1-859 <DIE>
A;Cross-references: EMBL:X61240; NID:g60256; PIDN:CAA43572.1; PID:g60257
C;Superfamily: type E retrovirus env polyprotein
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R;Becker, M.; Zorr, B.; Becker, A.; Habermehl, K.O.
Bubmitred to the EMBL Data Library, March 1995
A;Description: Molecular and phylogenetic characterisation of A;Reference number: S53091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 83; DB 2; Length 859
Pred. No. 0.0002;
6; Mismatches 7; Indels
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59.7%; Score 83; DB 2; Length 869
Best Local Similarity 50.0%; Pred. No. 0.0002;
Matches 13; Conservative 6; Mismatches 7; Indels
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A;Residues: 1-881 <CHA>
A;Cross-references: GB:Y00277; GB:M16403; NID:g61730
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Pred. No. 0.0002;
                                                                                                                                                                                                                                            submitted to the EMBL Data Library, August 1989
A;Reference number: S24571
A;Accession: S24571
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1 Similarity 50.0%;
13; Conservative
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Best Local Similarity
Matches 13; Conserv
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S53098
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C;Species: human immunodeficiency virus type 2, HIV-2
A/Note: host Homo appiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jun-2000
C;Accession: F38475; J00978
R;Tristem, M.; Hill, F.; Karpas, A.
J. Gen. Virol. 72, 721-724, 1991
A;Title: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus typ
A;Rccession: F38475; MUD:91170959; PMID:2005437
A;Accession: F38475; MUD:91170959; PMID:2005437
A;Accession: F38475
A;Molecule type: DNA
A;Recence under: A38475; MUD:91170959; PMID:2005437
A;Accession: F3859 cff1
A;Cross-references: GB:D00335; NID:93153166; PIDN:BAA00716.1; PID:9221472
C;Comment: The cleavage sites of this polyprotein have not been determined.
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Superfamily: type E retrovirus env polyprotein
C;Superfamily: signal sequence #status predicted <SIG>F;20-859/Product: env polyprotein #status predicted <SIG>F;20-859/Product: env polyprotein #status predicted <ENP>F;38,71,115,148,163,176,188,195,205,237,247,271,277,288,239,309,343,366,398,411,448,463;
                                                                                                                                                                Publication precursor - human immunodeficiency virus type 2 (isolate GH-1)

NyAlternate names: coat polyprotein

C;Species: human immunodeficiency virus type 2, HIV-2

A;Note: host Homo sapiens (man)

C;Date: 30-Jun-1990 #sequence_revision 26-Jan-1996 #text_change 16-Feb-1997

C;Accession: JS0334

A;Title: Sequence of a distinct HIV-2 isolate from Ghana showing significant divergence

A;Reference number: JS0327; MUID: 90122350; PMID: 2611042

A;Reference number: JS0327; MUID: 90122350; PMID: 2611042

A;Residues: 1-852 - HAA>

A;Residues: 1-852 - HAA>

A;Note: this sequence was submitted to JIPID, October 1989

A;Note: this sequence was submitted to JIPID, October 1989

A;Note: this sequence was submitted to JIPID, October 1989

A;Note: this sequence was submitted to JIPID, October 1989

A;Note: this sequence was submitted to JIPID, October 1989

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A;Note: this sequence was submitted to JIPID, October 1989

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A;Note: this sequence was submitted to JIPID, October 1989

A;Note: this sequence was submitted to JIPID, October 1989

A;Note: this sequence was submitted to JIPID, October 1989

A;Note: this sequence was submitted to JIPID, Oc
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   RVTAIEKYLKDQAQLNSWGCAFRQVC 593
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569 RVTAIEKYLKDQAQLNSWGCAFRQVC 594
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579 RVTAIEKYLKDQAQLNSWGCAFRQVC 604
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C,Accession: T11566
R;Hirsch, V.M.; Adger-Johnson, D.; Cambell, B.; Goldstein, S.; Brown, C.; Elkins, W.R.; V.J. 1608-1620, 1997
A;Title: A molecularly cloned, pathogenic, neutralization-resistant simian immunodeficie A;Reference number: Z17285; MUID:97151152; PMID:8995688
A;Accession: T11566
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C;Species: simian immunodeficiency virus SIVagm
C;Date: 03.Feb-1994 #sequence_revision 03-Feb-1994 #text_change 26-Aug-1999
C;Accession: G46356; G36660
R;Baier, M.; Garber, C.; Mueller, C.; Cichutek, K.; Kurth, R.
R;Baier, M.; Garber, C.; Mueller, C.; Cichutek, K.; Kurth, R.
A;Title: Complete nucleotide sequence of a simian immunodeficiency virus from African gr
A;Reference number: A46356; MUID:90232731; PMID:2158689
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R;Fukasawa, M.; Miura, T.; Hasegawa, A.; Morikawa, S.; Tsujimoto, H.; Miki, K.; Kitamura: Mature 313, 457-461, 1989
A;Title: Sequence of simian immunodeficiency virus from African green monkey, a new membia;Reference number: A30045; MUID:88232906; PMID:3374586
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C;Keywords: AIDS; capsid protein; coat protein; immunodeficiency; polyprotein; transmemb
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C;Species: simian immunodeficiency virus, SIV
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Oct-1997
                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-887 <HIR>
A;Cross-references: EMBL:U72748; NID:g1695908; PIDN:AAC56565.1; PID:g1695916
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A;Cross-references: GB-N30931; NID:g334400; PIDN:AAA91919.1; PID:g334407
A;Cross-references: GB-N30931; NID:g334407
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: polyprotein; transmembrane protein
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7; Indels
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Pred. No. 0.0004;
6; Mismatches 7; Indels
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Local Similarity 50.0%; Pred. No. 0.00028;
nes 13; Conservative 6; Mismatches 7; Indels
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C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; immunodeficiency
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Best Local Similarity 50.0%;
Matches 13; Conservative (
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ilarity 50.0%;
Conservative
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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Matches
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A) Species similar immunodeficiency virus SIVsm
A; Variety: strain 6.
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Accession: T11555
B; Hirsch, V.M.; Marrin, J.E.; Dapolito, G.; Elkins, W.R.; London, W.T.; Goldstein, S.; J. J. Virol. 68, 2649-2661, 1994
A; Hitle: Spontaneous substitutions in the vicinity of the V3 analog affect cell tropism A; Accession: T11555
A; Accession: T1155
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-886 *HIR>
A; Residues: 1-886 *HIR>
A; Cross-references: EMBL: U04985; NID: 9451609; PIDN: AAA18063.1; PID: 9451611
A; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: host Cercocebus torquatus atys (sooty mangabey)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-Aug-1999
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C;Species: simian immunodeficiency virus SIVsm
A;Variety: strain E543
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                     env polyprotein - simian immunodeficiency virus (mangabey isolate F236)
N;Contains: 120K glycoprotein; 40K glycoprotein
C;Species: simian immunodeficiency virus, SIV
                  6
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Pred. No. 0.0002;
6; Mismatches 7; Indels
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Pred. No. 0.0002;
6; Mismatches 7; Indels
              Indels
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    Mismatches
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Best Local Similarity 50.0%;
Matches 13; Conservative
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Best Local Similarity 50.0%;
Matches 13; Conservative
13; Conservative
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T11555
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RESULT 66

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C.Superfamily: type E retrovirus env polyprotein
Kreywords: AIDS, cappid protein; coat protein; immunodeficiency; polyprotein; transmem?
F;1-536/Product: coat protein gp120 #status predicted <GP1>
F;537-889/Product: coat protein gp32 #status predicted <GP2>
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C;Species is simian immunodeficiency virus, SIV
C;Species is simian immunodeficiency virus, SIV
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Nov-1999
C;Accession: 828084
C;Accession: 828084
C;Arsubjmocto, H.; Hasegawa, A.; Maki, N.; Fukasawa, M.; Miura, T.; Speidel, S.; Cooper, Nature 341, 539-541, 1989
A;Title: Sequence of a novel simian immunodeficiency virus from a wild-caught African m
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A; Title: Genome organization and transactivation of the human immuno-deficiency virus t; A; Reference number: A26262; MUID:87173056; PMID:3031510
A; Concents: proviral DNA
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A;Cross-references: EMBL:X15781
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1989
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C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
A;Accession: S55069
A;Molecule type: DNA
A;Residues: 848-899 <WHF>
A;Cross-references: EMBL:X86731; NID:g840895; PIDN:CAA60408.1; PID:g861130
A;Experimental source: developmental stage week 45
A;Accession: S55070
                                                                                                                                                                                                                                                                                                                                                     A Cross-references: EMBL:X86725; NID:g840897; PIDN:CAA60196.1; PID:g861134 A;Experimental source: developmental stage week 8 A;Accession: S55071 A;Accession: S55071 A;Molecule type: DNA A;Cocession: 848-889 «WHY» A;Cross-references: EMBL:X86730; NID:g840894; PIDN:CAA60406.1; PID:g861128 A;Experimental source: developmental stage week 41
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Pred. No. 0.00058; Tr Indels
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50.0%;
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Best Local Similarity 50.0,
These 13; Conservative
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A; Residues: 848-889 < WHZ>
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A,Gene: env
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: C26737
A;Molecule type: DNA
A;Coss=references: GB:M19499; NID:g334657
C;Genetics:
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C;Genetics: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; polyprotein
C;Keywords: AIDS; capsid protein gpi20 #status predicted <GPS>
F;1-527/Product: coat protein gpi21 #status predicted <GPS>
F;268-735/Product: coat protein gpi23 #status predicted <GPS>
F;368-735/Product: hypothebical env-extn protein #status predicted <GFN>
F;376-880/Product: hypothebical env-extn protein #status predicted <ETN>
F;37,70.114,148,173,186,200,204,214,246,249,280,286,297,308,318,373,379,462,478,627,636,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Contains: coat protein appl20; coat protein gp32
N;Contains: coat protein gp120; coat protein gp32
N;Contains: coat protein gp120; coat protein gp32
C;Species: simian immunodeficiency virus, SIV
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text change 16-Jul-1999
C;Accession: D28873; S55074; $55068; S54796; S55069; S55071
R;Franchini, G.; Gurgo, C.; Guo, H.G.; Gallo, R.C.; Collalti, E.; Fargnoli, K.A.; Hall, Altile: Sequence of simian immunodeficiency virus and its relationship to the human imm A;Reference number: A28873; MUID:87287229; PMID:3497350
                                                                                                                                                                                                                                                                                                                                                              isolate STLV-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: C26737
R;Hirsch, V.; Riedel, N.; Mullins, J.I.
R1149, 307-319, 1987
A;Title: The genome organization of STLV-3 is similar to that of the AIDS virus except A;Reference number: A26737; WUID:87187627; PMID:3646094
                                                                                                                                                                                                                                                                                                                                                     nv polyprotein precursor - simian immunodeficiency virus SIVagm (type 3, isolate (Contains: coat protein gpl20; coat protein gp32; hypothetical protein env-extn 'Species: simian immunodeficiency virus SIVagm | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 1940 | 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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A,Molecule type: DNA
A)Residues: 1-889 <FRA
A)Cross-references: EMBL:M19499
R;Whatmore, A.; Cook, N.; Hall, G.; Sharpe, S.; Rud, E.; Cranage, M.
submitted to the EMBL Data Library, April 1995
A;Description: Repair and evolution of nef in vivo modulates SIV virulence.
A;Reference number: S54796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Accession: S55074
A; Molecule type: DNA
A; Residues: 847-889 < WHA>
A; Cross-references: EMBL:X86729; NID:g840893; PIDN:CAA60404.1; PID:g861126
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A; Accession: S55068
A; Molecule type: DNA
A; Residues: 8489 < WH2>
A; Residues: 8489 < WH2>
A; Residues: BMBL:X86724; NID:g840887; PIDN:CAA60394.1; PID:g840888
A; Experimental source: developmental stage week 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: S54796
A;Molecule type: DNA
A;Residues: 848-889 <WHW>
A;Cross-references: EMBL:X86726; NID:g840886; PIDN:CAA60398.1; PID:g861120
A;Experimental source: developmental stage week 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.3%; Score 81; DB 1; Length 880 ilarity 46.2%; Pred. No. 0.00041; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
                                                                                            :: |:|:|||| | |||: ::|
594 KVTAIEKYLKDQAQLNAWGCAFRQVC 619
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Best Local Similarity
Matches 12; Conserv
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A; Accession: C26262

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A; Molecule type: DNA
A; Mesidues: 1-688 cGUy>
A; Residues: 1-688 cGUy>
A; Residues: 1-688 cGUy>
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C; Genetics:
A; Gene: en.
C; Genetics:
C;
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